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(54) Title: 87 HUMAN SECRETED PROTEINS					
(57) Abstract					
<p>The present invention relates to 87 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>					

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87 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and
5 their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or
10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum
15 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

Proteins targeted to the ER by a signal sequence can be released into the
20 extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or
25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include
30 the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using
35 secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard,
5 Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained
10 in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the
15 filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages
20 of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even
25 lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include
30 Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such
35 as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be
10 single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability
15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

 The polypeptide of the present invention can be composed of amino acids joined
20 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,
25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be
30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a
35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

The translation product of this gene shares sequence homology with nucleolin, which is thought to be important in macromolecule binding, as well as some membrane proteins. Preferred polypeptide fragments comprise the amino acid sequence:
 DPEAADSGEPQNKRTDLP EEEYVKEEIQENEEAVKKMLVEATREFEEVVDES
 (SEQ ID NO:239); QKLKRKAEDPEAADSGEPQNKRTDLP EEEYVKEEIQENEE
 AVKKMLVEATREFEEVVDES (SEQ ID NO:240); KAMEKSSLTQHSWQSLKDR
 YLKHLRGQEHKYLLGDAPVSPSSQKLKRKAEDPEAADSGEPQNKRTDLP
 EEEYVKEEIQENEEAVKKMLVEATREFEEVVDESPPDFEIH (SEQ ID NO:241).
 Also preferred are the polynucleotide fragments encoding these polypeptide fragments.

This gene maps to chromosome 16, and therefore can be used as a marker in linkage analysis for chromosome 16.

This gene is expressed primarily in brain and kidney and to a lesser extent in wide range of tissues.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cell-cell interaction or cell-matrix interaction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
10 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and kidney, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and kidney, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
15 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:125 as residues: Met-1 to Trp-10.

The tissue distribution and homology to nucleolin indicates that polynucleotides
20 and polypeptides corresponding to this gene are useful for treatment/diagnosis of diseases involving cell-cell interaction or cell-extracellular matrix interaction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

The translation product of this gene shares sequence homology with a porcine
25 zona pellucida protein ZPDS.1711. (See Accession No. R39356.) These two proteins have weak homology with *Drosophila* commissureless and metal homeostasis proteins which are thought to be important in controlling growth cone guidance across the CNS midline and protecting cells against reactive oxygen toxicity. thus, based on homology, it is likely that this gene also be involved in development. Preferred polypeptide
30 fragments comprise the amino acid sequence: LPSYDEAERTKAEATIPLVGRDEDF VGRDDFDDADQLRIGNDGIFMLTFFMAFLFNWIGFFLSFCLTTSAAGRYGAISG FGLSLIKWILIVRFSTYFPGYFDGQYWLWWVFLVLGFLFLRGFINYAKVRKM PETFSNLPRTRVLFI (SEQ ID NO:242); and/or AGRYGAISGFGLSLIKWILIVRFS (SEQ ID NO:243). Also preferred are polynucleotide fragments encoding these
35 polypeptide fragments. This gene maps to chromosome 5, and therefore can be used in linkage analysis as a marker for chromosome 5.

This gene is expressed primarily in kidney, adrenal gland, brain and to a lesser extent in wide range of tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, fertilization control or tissue damages by metabolites or other toxic agents. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and urosecretion system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., kidney, adrenal gland, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to zona pellucida protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for fertility control such as contraceptive development. The homology with metal homeostasis and commissureless genes indicates the gene's function in spermatozoa guidance and protection. It would also be useful for the treatment/diagnosis of tissue damages caused by toxic metabolites and other agents since the gene product is also expressed in urosecretive tissues.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 3**

This gene is expressed primarily in liver and to a lesser extent in placenta. Preferred polypeptide fragments comprise the amino acid sequence: MKHLSAWNFT KLTLFLQLWEI FEGSVENCQTLTSYSLQIKYTFSRGSTFYI (SEQ ID NO:244). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, digestive and nutrient transport/utilization disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive and

circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., liver, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in liver and placenta indicates that the protein product is either an extracellular enzyme or a molecule carrier. Therefore, polynucleotides and polypeptides corresponding to this gene are useful for diagnosis/treatment of digestive and nutrient transport/utilization disorders, including malabsorption and malnutrition.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene shares homology with the sap47 gene of *Drosophila melanogaster*, a gene which codes for a conserved neuronal protein associated with synaptic terminals. (See Mol. Brain Res. 32:45-54 (1995); see also, Accession No. 929571.) Thus, based on homology, the gene of the present invention also should be associated with synaptic terminals. Preferred polypeptide fragments comprise the amino acid sequence:
 FSSDFRTSPWESRRVESKATSARCGLWGSGPRRRPASGMFRGLSSWLGLQQP
 VAGGGQPNGDAPPEQPSETVAESAEEELQQAGDQELLHQAKDFGNLYLNFASA
 ATKKITESVAETAQTIKKSVEEGKIDGIIDKTIIGDFQKEQKKFVEEQHTKKSEA
 AVPPWVDTNDEETIQQQILALSADKRNFLRDPPAGVQFNFDQMYPVVALVML
 (SEQ ID NO:245); MRFALVPKLVKEEVFWRNYFYRVSLIKQSAQLTALAAQQQA
 AGKGGEEQ (SEQ ID NO:246); STSPGVSEFVSDAFDACNLNQEDLRKEMEQL
 VLDKKQEETAVLEEDSADWEKELQQELQEYEVVTESEKRDENWDK (SEQ ID
 NO:247); SPWESRRVESKATSARCGLWGSGPRRRPASGMFRGLSSWLGLQQ
 PVAGGGQPNGDAPPEQPS (SEQ ID NO:248); PVAGGGQPNGDAPPEQPSETV
 ESAEEELQQAGDQELLHQAKDFGNLYLNFASAATKKITESVAE (SEQ ID NO:
 249); and/or FQKEQKKFVEEQHTKKSEAAVPPWVDTNDEETIQQQILALSADKR
 NFLRDPPAGVQFNFDQMYPVVALVML (SEQ ID NO:250). Also preferred are
 polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in kidney pyramids and to a lesser extent in lung and other tissues of various types. This gene fluxes calcium in human aortic smooth muscle cells, and therefore is involved in signal transduction.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, renal and nervous disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the kidney and/or nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., kidney, lung, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in kidney and lung and homology with sap47 indicates that the protein product has regulatory or direct functions in molecular exchange with body fluids and nervous system signaling. Polynucleotides and polypeptides corresponding to this gene are useful for treatment of disorders in kidney and nervous system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 5

The translation product of this gene shares sequence homology with the mouse Ly-9.2 antigen which is thought to be an important cell surface marker in lymphoids, myeloids and hematopoietic progenitors. (See Accession No. gil198932.) Preferred polypeptide fragments comprise the amino acid sequence: PFICVARNPVSRNFSSPI LARKLCEGAA (SEQ ID NO:251); and/or KEDPANTVYSTVEIPKKMENPHSLT MPDTPRL (SEQ ID NO:252). Also preferred are polynucleotide fragments encoding these polypeptide fragments. Based on homology, it is likely that this gene is also a cell surface marker, involved in hematopoiesis.

This gene is expressed primarily in activated macrophages, monocytes and T-cells and to a lesser extent in spleen and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., blood cells, and bone marrow, and cancerous and wounded

tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:129 as residues: Lys-26 to Tyr-33, Arg-44 to Ile-49, Ser-53 to Lys-71, Lys-86 to Pro-91.

The tissue distribution and homology to Ly-9.2 surface immunoglobulin family indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of immune and hematopoietic disorders. Polypeptides and polynucleotides corresponding to this gene are also be used as a marker for leukemia or a modulator of the functions of the cells of macrophage/monocyte or T-cell types.

FEATURES OF PROTEIN ENCODED BY GENE NO: 6

The translation product of this gene shares sequence homology with the *Drosophila* glutactin gene which is thought to be important in cell-cell interaction or cell-extracellular matrix contact.

This gene is expressed primarily in colon tissue, aorta endothelial cells and to a lesser extent in skin, breast tissue and T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of these tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the gastrointestinal tract, vascular system or T-cell development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, cardiovascular system, and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., colon, cardiovascular tissue, skin, mammary tissue, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to glutactin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the development and maintenance of the integrity of the basal membrane in the gastrointestinal tract and

cardiovascular system. The expression in T-cells also indicate the protein may be involved in T-cell adhesion, cell-cell interaction and development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

The translation product of this gene shares sequence homology with MURF4 protein, an ATPase homolog, which is thought to be important in ATP hydrolysis.

This gene is expressed primarily in breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, breast cancer and non-neoplastic breast diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to MURF4 gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neoplastic or non-neoplastic breast diseases because ATPase like protein may be involved in changed metabolic states of the breast.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

This gene shares homology to the alcohol dehydrogenase gene. Preferred polypeptide fragments comprise the amino acid sequence: ASAVLLDLPNSG GEAQAKKLGNNCVFAPADVTSEKDVQTALALAKGKFGVRVDVAVNCAGIAVAS KTYNLKKGQTHTLEDFQRVLDVNLMTFNVIRLVAGEMGQNEPDQGGQRGVI INTASVAAFEGQVGQAAYSASKGGIVGMTLPIARDLAPIGIRVMTIAPGLFGTPL LTSLPEKVCNFLASQVPFPSRLGDPAEYAHLVQAIENPFLNGEVIRLDGAIRMQ P (SEQ ID NO:253); and/or SVAAFEGQVGQAAYSASKGGIVGMTLPIA (SEQ ID NO:254). Polynucleotides encoding these fragments are also encompassed by the invention. Other groups have also recently cloned this gene, recognizing its homology to alcohol dehydrogenase. (See Accession No. 1778355.) Moreover, a second group

recently cloned the mouse homologue of this gene. (See Accession No. 2078284.) They found that the mouse homologue binds to amyloid beta-peptide and mediates neurotoxicity in Alzheimer's disease, calling the protein ERAB. This gene maps to chromosome X, and therefore can be used in linkage analysis as a marker for chromosome X. Therefore, mutations in the translated product of this gene may be involved in Alzheimer's disease in humans, as well as other sex linked diseases. This gene can be used as a diagnostic marker for these diseases.

Preferred epitopes include those comprising a sequence shown in SEQ ID NO:132 as residues: Arg-45 to Ser-53.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

The translation product of this gene shares weak sequence homology with rat N-methyl-D-aspartate receptor subunit and other proline-rich proteins which are thought to be important in neurotransmission or protein-protein interaction.

This gene is expressed primarily in synovial hypoxia and to a lesser extent in ovary, senescent cells and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, synovial hypoxia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the synovia and brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., synovial tissue, ovary and other reproductive tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in synovial hypoxia and nerve tissues, and homology to N-methyl-D-aspartate receptor subunit and other proline-rich proteins indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of synovial hypoxia and other synovial disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in prostate and to a lesser extent in placenta and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male and female infertility, cancer, and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system and neoplasia, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., prostate, placenta, ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:134 as residues: Pro-17 to Met-23, Ala-30 to Trp-38, Ile-49 to Trp-54, Lys-68 to Gly-74, Thr-93 to Gly-99, Met-126 to Glu-132, Gly-173 to Ser-178, Lys-205 to Tyr-214.

The tissue distribution of this gene in the prostate, placenta and ovary indicates that this gene product is useful for treatment/diagnosis of male or female infertility, endocrine disorders, fetal deficiencies, ovarian failure, amenorrhea, ovarian cancer, benign prostate hyperplasia, prostate cancer, and other forms of cancer of the reproductive system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

This gene is expressed primarily in the thyroid and to a lesser extent in the pineal gland. This gene maps to chromosome 10, and therefore can be used as a marker in linkage analysis for chromosome 10. Preferred polypeptide fragments comprise the amino acid sequence: HPIEWAINAATLSQFY (SEQ ID NO:256); CWIKYCLTLMQN AQLSMQDNIG (SEQ ID NO:257); KVSYLRLDFEARELFLLGQHYVF (SEQ ID NO:258); MERRCKMHKRXIAMLEPLTVDLNPQ (SEQ ID NO:259); and/or SHIV KKINNLNKSALKY YQLFLD (SEQ ID NO:260). Also preferred are polynucleotides encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as

reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, thyroid and pineal gland disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., thyroid and pineal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:135 as residues: Ser-2 to Ser-8, Thr-38 to Arg-44.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/detecting immune disorders such as arthritis, asthma, immune deficiency diseases (e.g., AIDS), and leukemia, as well as treating/detecting thymus disorders (e.g., Graves Disease, lymphocytic thyroiditis, hyperthyroidism, and hypothyroidism), and treating/detecting pineal gland disorders (e.g., circadian rhythm disturbances associated with shift work, jet lag, blindness, insomnia and old age).

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

This gene is expressed primarily in lung and tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, pulmonary or immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., pulmonary tissue, and tonsils, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily

fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:136 as residues: Glu-28 to Gly-49.

5 The tissue distribution of this gene only in lung indicates that it could play a role in the treatment/detection of lung lymphoma or sarcoma formation, pulmonary edema and embolism, bronchitis and cystic fibrosis. Its expression in tonsils indicates a potential role in the treatment/detection of immune disorders such as arthritis, asthma, immune deficiency diseases (e.g., AIDS), and leukemia, in addition to the treatment/detection of tonsillitis.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 13**

This gene is expressed primarily in lymphoid, myeloid and erythroid cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, myeloid cells, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The predominant tissue distribution of this gene in hematopoietic cell types indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma, immunodeficiency diseases and leukemia. Preferred embodiments of the present invention are polypeptide fragments comprising the amino acid sequence: FTHLSTCLLSLLLVRMSGFLLLARASPSI
30 CALDSSCFVEYCSSYSSSCFLHQHFPSLLDHLCQ (SEQ ID NO:261); or FLLL ARASPSICALDSSCFVQEY (SEQ ID NO:262). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

35 This gene is homologous to the *Drosophila Regena* (*Rga*) gene. (See Accession No. 1658504.) This *Drosophila* gene is thought to be a homolog of the global negative

transcriptional regulator NOT2 (CDC36) from yeast, which modifies gene expression and suppresses position effect variegation. Preferred polypeptide fragments comprise the amino acid sequence: PDGRVTNIPQGMVTDQFGMIGLLTFIRAAETDPGMVHL
 5 (SEQ ID NO:263); VHLALGSDLTTTLGLNLNSPENLYP (SEQ ID NO:265); EDLLFYLYYMNGGDVLQLLA VELFN RDWRYHKEERVWI TR (SEQ ID NO:264); and/or HNEDFPALPGS (SEQ ID NO:266).

This gene is expressed primarily in placenta and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
 10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurodegenerative and developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
 15 disorders of the above tissues or cells, particularly of the neurological system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 20 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:138 as residues: Leu-9 to Tyr-15, Asp-34 to Gln-46, Pro-51 to Asp-57, Gly-88 to Thr-104, Thr-123 to Ser-128.

25 The tissue distribution of this gene indicates that it could be used in the detection and/or treatment of neurological disorders such as such as Alzheimer's Disease, Parkinson's Disease, Huntington's Disease, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, and panic disorder.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 15**

This gene is expressed primarily in adrenal gland tumor and osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
 35 not limited to, endocrine and bone disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system and in bone, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adrenal gland, and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:139 as residues: Ile-52 to Trp-57.

The tissue distribution of this gene indicates that it may be involved in the treatment and/or detection of adrenal gland tumors, osteosarcomas, endocrine disorders and bone disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

The translation product of this gene shares sequence homology with the FK506 binding protein, a protein which plays an important role in immunosuppression. (See Accession No. M75099.) Specifically, a 12-kDa FK506-binding protein (FKBP-12) is a cytosolic receptor for the immunosuppressants FK506 and rapamycin. (See, Proc. Natl. Acad. Sci. 88: 6677-6681 (1991).) Thus, based on homology, it is likely that this gene also has immunosuppression activity. Preferred polypeptides comprise the amino acid sequence: GRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRRAIPSH LAYGKRGFPSPVPADAVVQYDVELIALIR (SEQ ID NO:267); and/or IHYTGSLV DGR IIDTS (SEQ ID NO:268). Also preferred are the polynucleotide fragments encoding these polypeptides.

This gene is expressed primarily in melanocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and cancer, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:140 as residues: Ala-118 to Phe-124, Arg-178 to Lys-201.

- 5 The tissue distribution and homology to the FK506 binding proteins which are believed to a role in immunosuppression mediated by the immunosuppressant drugs rapamycin and cyclosporin, indicates that this gene could serve as a novel target for the identification of novel immunosuppressant drugs.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 17**

- The translation product of this gene shares sequence homology with the rat calcium-activated potassium channel rSK3, which is thought to be important in regulating vascular tone. (See Accession No. gil2564072, gil1575663, and gil1575661.) Although homologous to these proteins, this gene contains an 18 amino
15 acid insert, not previously identified in the homologs. Preferred polypeptide fragments comprise the amino acid sequence: CESPESPAQPSGSSLPAWYH (SEQ ID NO:269). Also preferred are the polynucleotide fragments encoding these polypeptides.

 This gene is expressed primarily in B-cells, frontal cortex and endothelial cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiovascular (hyper/hypotension, asthma, pulmonary edema, pneumonia, heart disease, restenosis, atherosclerosis, stroke, angina and thrombosis) and neurological disorders. Similarly, polypeptides and antibodies directed to these
25 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, brain and other tissue of the nervous system, and endothelium,
30 and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
35 NO:141 as residues: Glu-72 to Gly-82, His-90 to Val-95, Gln-168 to Lys-174, Val-202 to Ser-212.

The tissue distribution and homology to calcium-activated potassium channels indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of vascular disorders (hyper/hypotension, athesma, pulmonary edema, pneumonia, heart disease, restenosis, atherosclerosis, stoke, angina and thrombosis).

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

This gene is expressed primarily in smooth muscle and to a lesser extent in brain (amygdala, corpus colosum, hippocampus).

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiovascular (hypertension, heart disease, athesma, pulmonary edema, restenosis, atherosclerosis, stoke, angina, thrombosis, and wound healing), and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular and neurological systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., smooth muscle, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:142 as residues: Lys-43 to Arg-49, Tyr-58 to Glu-65.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of cardiovascular disorders (hypertension, heart disease, athesma, pulmonary edema, restenosis, atherosclerosis, stoke, angina, thrombosis, and wound healing). Expression in brain indicates a role in the treatment and diagnosis of behavioral or neurological disorders, such as depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 19

This gene is expressed primarily in T-cells (Jurkats, resting, activated, and

anergic T-cells), endothelial cells, pineal gland, and to a lesser extent in a variety of other tissues and cell types. Preferred polypeptide fragments comprise the amino acid sequence: EEAGAGRRCSHGGARPAGLGNEGLGLGGDPDHTDTGSRSKQRINN WKESKHKVIMASASARGNQDKDAHFPFPPSKQSLLFCPKSKLHIHRAEISK
5 (SEQ ID NO:270); and/or SKQRINNWKESKHKVIMASASAR (SEQ ID NO:271). Also preferred are the polynucleotide fragments encoding these polypeptides.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
10 not limited to, inflammation, immune and cardiovascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neurological and vascular systems, expression of this gene at significantly higher or
15 lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, endothelial cells, and pineal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
20 fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:143 as residues: Phe-71 to Arg-76, Pro-82 to His-87, Glu-103 to Ala-111.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune
25 disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. In addition, expression in the pineal gland might suggest a role in the diagnosis of specific brain tumors and treatment of neurological disorders. Endothelial cell expression might suggest a role in cardiovascular or respiratory/pulmonary disorders or infections
30 (atherosclerosis, pulmonary edema, pneumonia).

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

This gene is expressed primarily in brain and embryo and to a lesser extent in leukocytes. This gene maps to chromosome 15, and therefore can be used as a marker
35 in linkage analysis to chromosome 15.

Therefore, polynucleotides and polypeptides of the invention are useful as

reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g. cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:144 as residues: Met-1 to Gly-8.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. The expression in the brain -- and in particular the fetal brain -- would suggest a possible role in the treatment and diagnosis of developmental and neurodegenerative diseases of the brain and nervous system (depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior).

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

This gene is expressed primarily in brain, kidney, lung, liver, spleen, and a variety of leukocytes (especially T-cells) and to a lesser extent in a variety of other tissues and cell types.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemias, lymphomas, autoimmune, immunosuppressive, and immunodeficiencies, hematopoietic disorders, as well as renal disorders, and neoplasms. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the renal, pulmonary, immune, and central nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,

brain and other tissue of the nervous system, kidney, pulmonary tissue, liver, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
5 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of renal conditions, such as acute renal failure, kidney fibrosis, and kidney tubule regeneration.
10 The expression in leukocytes and other immune tissues indicates a role in immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. The expression in the brain -- and in particular the fetal brain -- indicates a possible role in the treatment and diagnosis of developmental and neurodegenerative diseases of the
15 brain and nervous system (depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior).

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

This gene is expressed primarily in skin (fetal epithelium, keratinocytes and
20 skin). This gene also maps to chromosome 19, and therefore can be used in linkage analysis as a marker for chromosome 19.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
25 not limited to, skin cancers (e.g., melanomas), eczema, psoriasis or other disorders of the skin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skin, expression of this gene at significantly higher or lower levels
30 may be routinely detected in certain tissues (e.g., skin and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those
35 comprising a sequence shown in SEQ ID NO:146 as residues: Pro-28 to Glu-35, Ser-39 to Phe-44, Ala-94 to Gln-99.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of skin cancers (e.g., melanomas), eczema, psoriasis or other disorders of the skin.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 23

This gene maps to chromosome 11. Another group recently isolated this same gene, associating the sequence to the region thought to harbor the gene involved in Multiple Endocrine Neoplasia Type 1, or MEN 1. (See Accession No. 2529721 and Genome Res. 7(7), 725-735 (1997), incorporated herein by reference in its entirety.)

10 Preferred polypeptide fragments comprise the amino acid sequence: LFHWACLNERA AQLPRNTAXAGYQCPSCNGPS (SEQ ID NO:272).

This gene is expressed primarily in epididymus, pineal gland, T-cells, as well as fetal epithelium, lung and kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as
15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune, metabolic mediated disorders, and MEN. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
20 number of disorders of the above tissues or cells, particularly of the immune, renal, neurological and pulmonary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., epididymus and other reproductive tissue, pineal gland, T-cells and other blood cells, epithelium, lung, and kidney, and cancerous and wounded tissues) or bodily fluids
25 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for the treatment and diagnosis of developmental deficiencies or abnormalities as well as a host of different disorders which arise as a result of conditions in the indicated tissues or cell types. An area of particular interest is in the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g.
35 AIDS) and hematopoietic disorders. The expression in the brain, and in particular the fetal brain, would suggest a possible role in the treatment and diagnosis of

developmental and neurodegenerative diseases of the brain and nervous system (depression, schizophrenia, Alzheimer's disease, mania, dementia, paranoia, and addictive behavior). Respiratory/pulmonary disorders, such as atesma, pulmonary edema are also potential therapeutic areas, as well as renal conditions such as acute renal failure, kidney fibrosis and kidney tubule regeneration. Moreover, this gene can be used in the treatment and/or detection of MEN I.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

This gene is expressed primarily in fetal spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, leukemia, lymphoma, AIDS, hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., spleen and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

A closely related homolog of this gene was recently cloned by another group, calling the gene CDO, an oncogene-, serum-, and anchorage-regulated member of the Ig/fibronectin type III repeat family. (See Accession No. 2406628, and J. Cell Biol. 138(1): 203-213 (1997), herein incorporated by reference in its entirety.) Preferred polypeptide fragments comprise the amino acid sequence: FYTYRPTDSDNDSYKK DMVEGDKYWHISHLQPETSYDIKMQCFNEGGESEFSNVMICETKARKSSGQP GRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIIVLITFIPF CLWRAWKQKHTTDLGFPRSA LPPSCPYTMVPLGGLPGHQA VDSPTSVASVD

GPVLM (SEQ ID NO:273); or YIYYRPTSDSDNDSDYKKDMVEGDKYWHSISHLQ
PETSYDIKMQCFNEGGSEFSNVMICETKARKS (SEQ ID NO:274).

This gene is expressed primarily in fetal lung and kidney, human embryo and
osteoclastoma stromal cells and to a lesser extent in a variety of other tissues and cell
types.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, developmental disorders and cancers, as well as pulmonary and renal
disorders. Similarly, polypeptides and antibodies directed to these polypeptides are
useful in providing immunological probes for differential identification of the tissue(s)
or cell type(s). For a number of disorders of the above tissues or cells, particularly of
the respiratory/pulmonary, skeletal and renal systems, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
types (e.g., lung, kidney, embryonic tissue, and bone cells, and cancerous and
wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
fluid) or another tissue or cell sample taken from an individual having such a disorder,
relative to the standard gene expression level, i.e., the expression level in healthy tissue
or bodily fluid from an individual not having the disorder. Preferred epitopes include
those comprising a sequence shown in SEQ ID NO:149 as residues: Thr-5 to Pro-18,
Ala-76 to Thr-84.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for the detection and treatment of: osteoporosis,
fracture, osteosarcoma, ossification, and osteonecrosis, as well as
respiratory/pulmonary disorders, such as atesma, pulmonary edema, and renal
conditions such as acute renal failure, kidney fibrosis and kidney tubule regeneration.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

This gene is homologous to the HIV envelope glycoprotein. (See Accession
No. 2641463.) Preferred polypeptide fragments comprise the amino acid sequence:
NVRALLHRMPEPPKINTAKFNNNKRKNLSL (SEQ ID NO:275).

This gene is expressed primarily in pineal gland and skin, and to a lesser extent
in lung.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, neurological and behavior disorders; respiratory/pulmonary disorders, such as atesma, pulmonary edema; skin conditions such as eczema, psoriasis, acne and skin cancer, as well as AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
5 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous and respiratory systems, as well as skin and AIDS, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, pineal gland, epidermis, and pulmonary tissue, and cancerous and wounded tissues) or bodily fluids
10 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:150 as residues: Gln-15 to Gln-20.

15 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions which affect the above tissues, such as: skin cancer, eczema, psoriasis, acne, atesma, pulmonary edema, neuro-degenerative or developmental disorders such as Alzheimer's, depression, schizophrenia, dementia, and AIDS.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 27

Preferred polypeptide encoded by this gene comprise the following amino acid sequence: NTNQREALQYAKNFQPFALNHQKDIQVLMGSLVYLRQGIENSPYVHL
LDANQWADICDIFTRDACALLGLSVESPLSVSFSAGCVALPALNIKAVIEQRQC
25 TGVWNQKDELPIEVDLGGKCKWYHSIFACPILRQQTTDNNPPMKLVCGHIISRD
ALNKMFMNGSKLKCPYCPMEQSPGDAKQIFF (SEQ ID NO:276). Polynucleotides encoding such polypeptides are also provided as are complementary polynucleotides thereto.

This gene is expressed primarily in liver (adult and fetal) and spleen tissue, and
30 to a lesser extent in placenta, T helper cells, kidney tumor, ovarian tumor, melanocytes and fetal heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
35 not limited to, immune and developmental diseases and disorders and liver diseases such as liver cancer. Similarly, polypeptides and antibodies directed to these

polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, circulatory and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, placenta, blood cells, kidney, ovary and other reproductive tissue, melanocytes, and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of growth, hematopoietic and immune system disorders particularly related to the liver.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 28**

The translation product of this gene shares sequence homology with prostaglandin transporter which is thought to be important in metabolic and endocrine disorders. See, for example, Gastroenterology Oct:109(4):1274-1282 (1995). Preferred polypeptides encoded by this gene comprise the following amino acid sequence:

20 SYLSACFAGCNSTNLTGCACLTTVPAENATVVPGKCPSPGCQEAFLTFLCVMCI
CSLIGAMARHP (SEQ ID NO:277); and/or PSVIIIIRTVSPELKSYALGVLFLLRL
LGFIPPLIFGAGIDSTCLFWSTFCGEQGACVLYDNVVYRYLYVSIAIALKSFAFI
(SEQ ID NO:278).

This gene is expressed primarily in hematopoietic and brain tissues.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolic, immune and endocrine diseases and disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic, immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., endocrine tissue, hematopoietic tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to prostaglandin (and anion) transporter indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of endocrine, metabolic, immune and kidney disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed primarily in early stage human lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, growth and respiratory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the developmental and respiratory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:153 as residues: Val-50 to Trp-55.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of respiratory and growth diseases and disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

The translation product of this gene shares sequence homology with human DNA helicase which is thought to be important in accurate and complete DNA replication in creation of new cells. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: QSLFTRFVRVGVPTVDLDAQGRARA SLCXXYNWRYKNLGNLPHVQLLPEFSTANAGLLYDFQLINVEDFQGVGESEPN PYFYQNLGEAEYVVALFMYMCLLGYPADKISILTTYNGQKHLIRDIINRRCGNN PLIGRPNKVTTVDRFQGGQNDYILLSVRTRAVGHRLDVRRLVVAMSRAR (SEQ ID NO:279); and/or LVKEAKIIAMTCTHAALKRHDLVKLGFKYDNILMEE AAQILEIETFIPLLLQNPQDGFSRLKRWIMIGDHHQLPPVI (SEQ ID NO:280).

This gene is expressed primarily in testes tumor and to a lesser extent in adrenal

gland tumor and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers and endocrine/growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine, developmental, and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., testes and other reproductive tissue, adrenal gland, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to DNA helicase indicates that the protein products of this gene are useful for study, treatment, and diagnosis of many cancer types, including testicular cancer; as well as disorders involving endocrine function and normal growth and development.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 31

The translation product of this gene shares sequence homology with BID-apoptotic death gene (mouse), Genbank accession no. PID g1669514, which is thought to be important in programmed cell death.

25 This gene is expressed primarily in jurkat membrane bound polysomes and activated neutrophils and to a lesser extent in endothelial cells and human cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancers and other proliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, endothelium, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

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urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
5 NO:155 as residues: Glu-4 to Leu-11, Cys-28 to Arg-35, Gln-50 to His-66, Glu-73 to Gln-79, Gly-94 to Ser-100, Arg-114 to Asp-126, Pro-139 to Lys-146.

The tissue distribution and homology to BID-apoptotic death gene indicates that the protein products of this gene are useful for study of cell death, and treatment and diagnosis of proliferative disorders and cancers. Apoptosis - programmed cell death - is
10 a physiological mechanism involved in the deletion of peripheral T lymphocytes of the immune system, and its dysregulation can lead to a number of different pathogenic processes. Diseases associated with increased cell survival, or the inhibition of apoptosis, include cancers (such as follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, such as breast cancer, prostate cancer,
15 Kaposi's sarcoma and ovarian cancer); autoimmune disorders (such as systemic lupus erythematosus and immune-related glomerulonephritis rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and adenoviruses), inflammation; graft vs. host disease, acute graft rejection, and chronic graft rejection. Diseases associated with increased apoptosis include AIDS; neurodegenerative disorders (such as
20 Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration); myelodysplastic syndromes (such as aplastic anemia), ischemic injury (such as that caused by myocardial infarction, stroke and reperfusion injury), toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia. Thus, the invention provides a method of enhancing
25 apoptosis in an individual by treating the individual with a polypeptide encoded by this gene.

FEATURES OF PROTEIN ENCODED BY GENE NO: 32

30 The translation product of this gene shares sequence homology with human fructose transporter which is thought to be important in normal metabolic function and activity.

This gene is expressed primarily in T-cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, leukemia and other cancers, and metabolic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic, lymph and metabolic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:156 as residues: Pro-22 to Gly-48, Ser-54 to Pro-61.

The tissue distribution indicates that the protein products of this gene are useful for study of mechanisms leading to cancer, treatment and diagnosis of cancerous and pre-cancerous conditions; as well as the study and treatment of various metabolic diseases and disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 33

This gene is expressed primarily in human meningioma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and other disorders of the CNS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., meningioma and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:157 as residues: Asn-23 to Pro-31.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of disorders of the CNS and inflammatory responses.

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

This gene is expressed primarily in activated monocytes and wound healing tissues and to a lesser extent in fetal epithelium.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and inflammatory disorders and wound healing and tissue repair dysfunctions. Similarly, polypeptides and antibodies directed to these polypeptides are
- 10 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, epithelial and gastrointestinal systems, and healing wounds, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., monocytes and other blood cells, and epithelium, and
- 15 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:158 as residues:
- 20 Ala-28 to Ala-33, Gly-35 to Glu-45.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis, study and treatment of immune and inflammatory disorders and wound healing dysfunctions.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 35**

This gene is expressed primarily in human osteosarcoma and prostate cancer.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
- 30 not limited to, skeletal and neoplastic conditions such as bone and prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and skeletal systems, expression of this gene at significantly higher or lower
- 35 levels may be routinely detected in certain tissues (e.g., bone, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial

fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:159 as residues:

5 Ser-14 to Gly-22, Leu-37 to Gln-43.

The tissue distribution indicates that the protein products of this gene are useful for diagnosis and treatment of skeletal disorders and cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

10 This gene encodes a protein which is highly homologous to a protein called congenital heart disease protein 5, presumably implicated in congenital heart disease (see Genbank PID g2810996).

This gene is expressed primarily in Hodgkin's lymphoma, erythroleukemia cells, and TNF activated synovial fibroblasts, to a lesser extent in ovarian cancer,
15 cerebellum, spleen, fetal liver and placenta and finally to a lesser extent in various other mesenchymal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
20 not limited to, cancer, immune, hematopoietic and cardiovascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, hematopoietic and cardiovascular systems, expression of this gene at significantly
25 higher or lower levels may be routinely detected in certain tissues and cell types (e.g., heart and other cardiovascular tissue, lymphoid tissue, blood cells, bone marrow, ovary and other reproductive tissue, brain and other tissue of the nervous system, spleen, liver, and mesenchymal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell
30 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:160 as residues: Lys-41 to Met-49, Gln-54 to Glu-59, Glu-76 to Thr-88.

35 The homology of this gene and translation product to congenital heart disease protein 5 indicates a role for this protein in the diagnosis, prognosis and/or treatment of

heart disease or other cardiovascular related disorders. In addition, predominant expression in cells associated with the immune and hematopoietic system indicates a role for this protein in the treatment, diagnosis and/or prognosis of immune and autoimmune diseases, such as lupus, transplant rejection, allergic reactions, arthritis, asthma, immunodeficiency diseases, leukemia, AIDS, thymus disorders such as Graves Disease, lymphocytic thyroiditis, hyperthyroidism and hypothyroidism, graft versus host reaction, graft versus host disease, transplant rejection, myelogenous leukemia, bone marrow fibrosis, and myeloproliferative disease. The protein could also be used to enhance or protect proliferation, differentiation and functional activation of hematopoietic progenitor cells such as bone marrow cells, which could be useful for cancer patients undergoing chemotherapy or patients undergoing bone marrow transplantation. The protein may also be useful to increase the proliferation of peripheral blood leukocytes, which could be useful in the combat of a range of hematopoietic disorders including immunodeficiency diseases, leukemia, and septicemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

This gene is expressed primarily in ovarian cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, urogenital neoplasias. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:161 as residues: Asn-22 to Asn-27.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of ovarian and other tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

The translation product of this gene shares sequence homology with zinc finger proteins.

This gene is expressed primarily in various fetal, cancer, and endothelial lines.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune and growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiovascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for study, diagnosis and treatment of immune and developmental conditions and cancer.
20

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

This gene is expressed primarily in fetal, infant, and adult brain and to a lesser extent in other brain and endocrine organs and blastomas.

Therefore, polynucleotides and polypeptides of the invention are useful as
25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, brain tumors and neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
30 disorders of the above tissues or cells, particularly of the nervous and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, endocrine tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an
35 individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the

disorder.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of brain cancer and other neurological disorders.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 40

The translation product of this gene shares sequence homology with vesicular glycoproteins and lectins. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: DTYPNEEKQQERVFPXXSAMVNNGSLSYDHER DGRPTELGGCXAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGV
 10 RLPRGYFYTSSITGDLSDNHDVISLKLFEFTVERTPEEE (SEQ ID NO:281);
 and/or LKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGA
 LWNRVPCFLRDWELQVHFKIHGQGKKNLHGDGLAIWYT (SEQ ID NO:282).

This gene is expressed primarily in infant brain and to a lesser extent in various normal and transformed neural, endocrine, and immune organs.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological and neurodevelopmental conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological
 20 probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hormonal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, endocrine tissue, and tissue and cells of the immune system, and cancerous and wounded tissues)
 25 or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:164 as residues: Pro-64 to Gly-71, Gly-
 30 94 to Leu-100, Thr-110 to Pro-116, Thr-135 to Arg-145, Glu-164 to Glu-171, Asp-204 to Asp-211, Arg-253 to His-261, Asn-312 to Tyr-323.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of mental retardation and other neurological disorders and neoplasias.

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene displays homology to the glycosyltransferase family, which catalyze the addition of sialic acids to carbohydrate groups which are present on glycoproteins.

This gene is expressed primarily in smooth muscle and to a lesser extent in
5 pineal gland, fetal liver, and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, gastrointestinal injury, inflammatory and neurodegenerative conditions.
10 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., smooth muscle, pineal gland,
15 liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those
20 comprising a sequence shown in SEQ ID NO:165 as residues: Ser-12 to Trp-21, Arg-24 to Pro-32, Asp-73 to Lys-82, Lys-90 to Ala-97.

The tissue distribution indicates that the protein products of this gene are useful for the study, diagnosis and treatment of neurodegenerative and growth disorders and gastrointestinal repair.
25

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

The translation product of this gene shares sequence similarity with metallothionein polypeptides. See, for example, Proc. Natl. Acad. Sci. U S A 1992 Jul 15:89(14):6333-6337. Metallothioneins are believed to inhibit neuronal survival among
30 other biological functions. Based on the sequence similarity (especially the conserved cysteine motifs characteristic of the metallothionein family) the translation product of this gene is expected to share certain biological activities with other members of the metallothionein polypeptide family. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: PGT LQCSALHHD PGCANCSRFCRD
35 CSPPACQC (SEQ ID NO:283).

This gene is expressed exclusively in placenta and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, liver, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to metallothionien indicates that the protein products of this gene are useful for diagnosis and treatment of immune and hematopoietic system disorders and neurological diseases, especially in fetal development.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 43

Preferred polypeptides encoded by this gene comprise the following amino acid sequence: FLYDVLMXHEAVMRTHQIQLPDPEFPS (SEQ ID NO:284).

This gene is expressed primarily in T-cells and synovial tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune system disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, and T-cells and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein products of this gene are useful for treatment and diagnosis of disorders of the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

5 The translation product of this gene shares sequence similarity with several methyltransferases (e.g., see Genbank gil1065505).

 This gene is expressed primarily in ovary, thymus, infant adrenal gland, tissues of the nervous system and the hematopoietic tissue, and to a lesser extent in adipose tissue and many other tissues.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of the reproductive system, the endocrine system, the hematopoietic system and the CNS. Similarly, polypeptides and antibodies directed to
15 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, endocrine, CNS and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., ovary and other reproductive tissue, thymus, adrenal gland,
20 brain and other tissue of the nervous system, hematopoietic tissue, and adipose tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
25 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:168 as residues: Ser-3 to Gly-12, Asp-19 to Arg-31, Tyr-70 to Tyr-77, Asn-130 to Lys-140, Pro-165 to Gln-170, Pro-192 to Lys-199, Leu-216 to Glu-227, Glu-254 to Phe-281.

 The tissue distribution and homology to methyltransferase indicates that the
30 protein products of this gene are useful for diagnosis and treatment of disorders of the CNS, the hematopoietic system and reproductive organs and tissues. For example, the abundant expression in the ovary may indicate that the gene product can be used as a hormone with either systemic or reproductive functions; as growth factors for germ cell maintenance and in vitro culture; as a fertility control agent; remedy for sexual
35 dysfunction or sex development disorders; diagnostics/treatment for ovarian tumors, such as serous adenocarcinoma, dysgerminoma, embryonal carcinoma,

choriocarcinoma, teratoma, etc; The expression in thymus may indicate its utilities in T-cell development and thus its applications in immune related medical conditions, such as infection, allergy, immune deficiency, tissue/organ transplantation, etc.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 45

The translation product of this gene shares sequence homology with cytochrome C oxidase which is thought to be important in metabolic function of cells. This gene has now recently been published as estrogen response gene. See Genbank accession no. AB007618 and Mol. Cell. Biol. 18 (1), 442-449 (1998). See also J Immunol. Mar 10 1:154(5): 2384-2392 (1995), where the mouse homologue was published and implicated in siliocis.

This gene is expressed primarily in adipose tissue, kidney and fetal brain and to a lesser extent in several other tissues and organs.

Therefore, polynucleotides and polypeptides of the invention are useful as 15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolic diseases involving especially adipose tissue, brain and kidney. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell 20 type(s). For a number of disorders of the above tissues or cells, particularly of the CNS and vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adipose tissue, kidney, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell 25 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:169 as residues: Thr-5 to Ser-14.

The tissue distribution and homology to cytochrome C oxidase, estrogen 30 response gene product and siliocis related gene product indicates that the protein products of this gene are useful for diagnosis and treatment of metabolic disorders in the CNS, adipose tissue and kidney, particularly siliocis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 46

35 The translation product of this gene shares sequence homology with reticulocalbin. See, for example, J. Biochem. 117 (5), 1113-1119 (1995). Based on the

sequence similarity, the translation product of this gene is expected to share certain biological activities with reticulocalbin, e.g., Ca^{++} binding activities. This gene product is sometimes hereinafter referred to as "Reticulocalbin-2".

5 This gene is expressed primarily in breast, endothelial cells, synovial, heart and smooth muscle cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the breast, vascular and skeletal/cardiac muscular system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast, vascular and skeleto-muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., 15 mammary tissue, endothelial cells, synovial tissue, heart and other cardiovascular tissue, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an 20 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:170 as residues: Gly-16 to Arg-32, Ala-42 to Asn-50, Glu-66 to Gln-76, Arg-85 to Gly-94, Thr-108 to Asp-115, Trp-121 to Gly-130, Leu-137 to His-144, Glu-155 to Lys-161, Asp-175 to Ser-180, Glu-209 to Gly-217, Glu-232 to Glu-237, Thr-243 to Asp-261, Glu-287 to Arg-295.

25 The tissue distribution indicates that the protein products of this gene are useful for diagnosis and treatment of diseases of the vascular and skeletal/cardiac muscular system. The homology of the gene with reticulocalbin indicates its biological function in regulating calcium store, a particularly important function in muscular cell types. The gene expression in the heart may indicate its utilities in diagnosis and remedy in heart failure, ischemic heart diseases, cardiomyopathy, hypertension, arrhythmia, etc. The abundant expression in the breast may indicate its applications in breast neoplasia and breast cancers, such as fibroadenoma, papillary carcinoma, ductal carcinoma, Paget's disease, medullary carcinoma, mucinous carcinoma, tubular carcinoma, secretory carcinoma and apocrine carcinoma; juvenile hypertrophy and gynecomastia, mastitis 30 and abscess, duct ectasia, fat necrosis and fibrocystic diseases, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 47

The translation product of this gene shares weak sequence homology with H⁺-transporting ATP synthase which is thought to be important in cell metabolism or signal transduction.

5 This gene is expressed only in testis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of some types of diseases and conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
10 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and hematopoietic tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine,
15 synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Since only one out of about a million expressed sequence tag is found in testes
20 indicates that its expression is low and selectively in testes. Since some of the genes only expressed in testes are usually expressed in brain or in certain induced hematopoietic cells/tissues, it is speculated that this gene to be expressed in brain or hematopoietic cells/tissues and is useful for diagnosis and treatment of disorders these systems.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

The translation product of this gene shares sequence homology with human polymeric immunoglobulin receptor (accession No.X73079) which is thought to be important in antibody recognition and immune defenses. In one embodiment,
30 polypeptides of the invention comprise the sequence GWYWCG (SEQ ID NO:285). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in placenta and to a lesser extent in corpus callosum and fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

not limited to, disorders of the immune system, e.g. autoimmune diseases and immunodeficiency. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:172 as residues: Tyr-37 to Cys-49, Gly-51 to Tyr-56, Lys-88 to Trp-93, Leu-130 to Glu-136.

The tissue distribution and homology to human polymeric immunoglobulin receptor indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, e.g. autoimmune diseases and immunodeficiencies.

FEATURES OF PROTEIN ENCODED BY GENE NO: 49

This gene is expressed in thymus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., thymus and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders, e.g. autoimmunity and immunodeficiency.

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

Preferred polypeptide encoded by this gene comprise the following amino acid sequence: MKVGARIRVKMSVKNKAHPVVSTHWRWPAEWPQMFLHLAQEPRTE

5 VKSRPLGLAGFIRQDSKTRKPLEQETIMSAADTALWPYGHGNREHQENELQKY
LQYKDMHLLDSGQSLGHTHTLQGSHNLTALNI (SEQ ID NO:286).

Polynucleotides encoding this polypeptide are also provided as are complementary polynucleotides thereto.

10 This gene is expressed primarily in adrenal gland, pituitary, T helper cells, and breast cells and to a lesser extent in a wide variety of tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of the some diseases and conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., adrenal gland, pituitary, T-cells and other blood cells, and mammary tissue, and cancerous and wounded tissues) or bodily fluids
20 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:174 as residues: Gln-39 to Ser-47, Arg-57 to Glu-67,
25 Tyr-82 to Gln-95.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of a wide range of disorders, such as immune and endocrine disorders.

30 FEATURES OF PROTEIN ENCODED BY GENE NO: 51

The translation product of this gene shares sequence homology with human Sop2p-like protein which is important in cytoskeleton structure. In one embodiment, polypeptides of the invention comprise the sequence SLHKNSVSQISVLSGGKAKCS QFCTTGMDGGMSIWDVKSLESALKDLKI (SEQ ID NO:287). Polynucleotides
35 encoding this polypeptide are also encompassed by the invention. This gene maps to chromosome 7. Therefore, polynucleotides of the invention can be used in linkage

analysis as a marker for chromosome 7.

This gene is expressed primarily in immune and hematopoietic tissues/cells and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, immunological and hematopoietic disorders and inflammation. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
10 number of disorders of the above tissues or cells, particularly of the immune and
hematopoietic systems, expression of this gene at significantly higher or lower levels
may be routinely detected in certain tissues and cell types (e.g., immune and
hematopoietic tissue/cells, and cancerous and wounded tissues) or bodily fluids (e.g.,
serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
15 taken from an individual having such a disorder, relative to the standard gene
expression level, i.e., the expression level in healthy tissue or bodily fluid from an
individual not having the disorder. Preferred epitopes include those comprising a
sequence shown in SEQ ID NO:175 as residues: Lys-49 to Gln-54, Ala-61 to Arg-66,
Lys-82 to Lys-87, Glu-126 to Val-133, His-136 to Ile-141, Glu-175 to Ser-187, Asp-
20 286 to Leu-296, Ala-298 to Ser-310.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of immunological,
hematopoietic, and inflammatory disorders, e.g, immunodeficiency, autoimmunity,
inflammation.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 52

The translation product of this gene shares sequence homology with
Caenorhabditis elegans R53.5 gene encoding a putative secreted protein without
known function.

30

This gene is expressed primarily in endothelial cells, brain and several highly
vascularized, and tumor tissues and to a lesser extent in other tissues.

35

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, aberrant angiogenesis and tumorigenesis. Similarly, polypeptides and
antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular and brain system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, brain and other tissue of the nervous
5 system, and vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
10 sequence shown in SEQ ID NO:176 as residues: Thr-43 to Asn-60, Thr-106 to Phe-115, Asp-122 to Arg-133, Arg-186 to Asp-192, Leu-211 to Lys-216.

The tissue distribution and homology to a *C. elegans* secreted protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of disorders in vascular or brain system, e.g. aberrant
15 angiogenesis, ischemia, neurodegeneration, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

In one embodiment, polypeptides of the invention comprise the sequence EASKSSHAGLDLFSVAACHRF (SEQ ID NO:288). Polynucleotides encoding this
20 polypeptide are also encompassed by the invention.

This gene is expressed primarily in T-cells and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
25 not limited to, lymphocytic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the lymphoid system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell
30 types (e.g., T-cells and other blood cells, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
35 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:177 as residues: Pro-3 to Thr-8, Arg-37 to Asp-46.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, treatment, and cure of lymphocytic disorders.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 54

The translation product of this gene shares sequence homology with secreted cartilage matrix protein, a major component of the extracellular matrix of nonarticular cartilage which is thought to be important in cartilage structure. In specific embodiments, polypeptides of the invention comprise the sequence: RCKKCTEGPI
 10 DLVFVIDGSKSLGEENFEVVKQF (SEQ ID NO:297); VTGIIDSLTISPKAARVGL
 LQYSTQVH (SEQ ID NO:290); TEFTLRNFNSAKDMKKA VAHMKYM (SEQ ID NO:291); GKGSMTGLALKHMFERSFTQGE GARPF (SEQ ID NO:292); STRVP
 RAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIE (SEQ ID NO:293);
 EELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALED S (SEQ ID NO:294);
 15 TQRLEEMTQRM (SEQ ID NO:295); PQGCPEQPLH (SEQ ID NO:296); and/or
 YMGKGSMTGLALKHMFERSFT (SEQ ID NO:289). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in placenta, infant brain, prostate, fetal lung and to a lesser extent in endometrium and fetal tissues.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, abnormal placenta and pregnancy, disorder and injury in brain, prostate, and vasculature. Similarly, polypeptides and antibodies directed to these polypeptides
 25 are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproduction, neuronal, and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., placenta, brain and other tissue of the nervous system, prostate, lung and
 30 endometrium, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution and homology to cartilage matrix protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis,

treatment, and cure of abnormalities in placenta and pregnancy, disorder and injury in brain, prostate, and vasculature.

FEATURES OF PROTEIN ENCODED BY GENE NO: 55

5 The translation product of this gene is the human ortholog of bovine and hamster CII-3, a succinate-ubiquinone oxidoreductase complex II membrane-intrinsic subunit, which is thought to be important in mitochondrial electron transport chain during metabolism. In specific embodiments, the polypeptides of the invention comprise MAALLLRHVGRHCLRAHFSPQLCIRNAVPLGTTAKEEMERFWNKNIG
10 SNRPLSPHITIYS (SEQ ID NO:298); VFPLMYHTWNGIRHLMWDLGKGLKIPQL YQSG (SEQ ID NO:299); MAALLLRHVGRHCLRAH (SEQ ID NO:300); VKSLCL GPALHTAKFAL (SEQ ID NO:301); VFPLMYHTWNGIRHLMWDLGKGL (SEQ ID NO:302).

 This gene is expressed in 8-week old early stage human.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, metabolism disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
20 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the [insert system where a related disease state is likely, e.g., immune], expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
25 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution and homology to indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, treatment, and cure of
30 metabolism disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

 This gene is expressed primarily in umbilical vein endothelial cells, human ovarian tumor cells, human meningioma cells, and human Jurkat membrane bound
35 polysomes. In specific embodiments, polypeptides of the invention comprise the amino acid sequence: RVWDVRPFAPKERCVKIFQGNV (SEQ ID NO:303); HNF EK NLL

RCSWSPDGSKIAAGSADRFVYV (SEQ ID NO:304); and/or WDTTSRRILYKLPG HAGSINEVAFHPDEPI (SEQ ID NO:305). Polynucleotides encoding these polypeptides are also encompassed by the invention.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation, immune and cardiovascular disorders and urogenital neoplasias. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of these tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neurological, urogenital, reproductive system and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, cells, endothelial cells, ovary and other reproductive tissue, meningioma, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:143 as residues: Phe-71 to Arg-76, Pro-82 to His-87, Glu-103 to Ala-111.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders including: leukemias, lymphomas, auto-immune, immuno-suppressive (e.g. transplantation) and immunodeficiencies (e.g. AIDS) and hematopoietic disorders. In addition, expression in ovarian tumor cells suggests that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of ovarian tumors, and other tumors and neoplasias. Further, endothelial cell expression suggests a role in cardiovascular or respiratory/pulmonary disorders or infections (asthma, pulmonary edema, pneumonia).

FEATURES OF PROTEIN ENCODED BY GENE NO: 57

The translation product of this gene shares sequence homology with type I collagen. In specific embodiments, the polypeptides of the invention comprise the sequence: GRIPAPAPSVAGPDSR (SEQ ID NO:309); VRGRTVLRPGLDAEPE LSPE (SEQ ID NO:306); EQRVLERKCLKKERKKEERQ (SEQ ID NO:307); ARRS

AELAWDYLCRWAQKHKNWRFQKTRQTWLLHMYDSKVPDEHFSTLLAYLE
GLQGR (SEQ ID NO:255); and/or RLREAGLVAQHPP (SEQ ID NO:308).

Polynucleotides encoding these polypeptides are also encompassed by the invention.

5 This gene is expressed primarily in epididymus, prostate cell line (LNCAP),
and pituitary gland; and to a lesser extent in many other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, abnormalities of the epididymus, prostate (especially prostate cancer),
10 and pituitary gland. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
particularly of the male reproductive system and neuroendocrine system, expression of
this gene at significantly higher or lower levels may be routinely detected in certain
15 tissues (e.g., epididymus and other reproductive tissue, prostate, and pituitary gland,
and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine,
synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
having such a disorder, relative to the standard gene expression level, i.e., the
expression level in healthy tissue or bodily fluid from an individual not having the
20 disorder.

The tissue distribution and homology to type I collagen, indicates that
polynucleotides and polypeptides corresponding to this gene are useful for diagnosis
and treatment of abnormalities of the epididymus, prostate (especially prostate cancer),
and pituitary gland.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

This gene is expressed primarily in the frontal cortex of the brain from a
schizophrenic individual.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions, which include, but are
not limited to, schizophrenia. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
35 particularly of the nervous system, expression of this gene at significantly higher or
lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of

the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of schizophrenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

The polypeptide encoded by Gene 59 is homologous to human surface 4 integral membrane protein. In specific embodiments, the polypeptides of the invention comprise the sequence: TGCVLVLSRNFVQYACFGLFGIILQTIAYSILWDLKF LMRN (SEQ ID NO:310); SRSEGKSMFAGVPTMRESSPKQYMQLGGRVLLV LMFMTLLHFDASFFSIVQNIVG (SEQ ID NO:311); GTAEDFADQFLRVTKQYLP HVARLCLISTFLEDGIRMFQWSEQRDYIDTTWNCGYLLAS (SEQ ID NO:312); LMRNESRS (SEQ ID NO:314); ASFLLSRTSWGTA (SEQ ID NO:315); and/or ASFLLSRTSWGTA LMIL (SEQ ID NO:313). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in Hodgkin's lymphoma and lung; and to a lesser extent in many other human tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, Hodgkin's lymphoma, tumors or other abnormalities of the lung.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and respiratory systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., lymphoid tissue, and pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:183 as residues: Met-20 to Trp-27.

The tissue distribution indicates that polynucleotides and polypeptides

corresponding to this gene are useful for diagnosis and treatment of Hodgkin's lymphoma, tumors or other abnormalities of the lung.

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

5 This gene is expressed primarily in bone cancer and stomach cancer, and to a lesser extent in many other tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
10 not limited to, bone cancer and stomach cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, and the stomach, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues
15 (e.g., bone, and stomach, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of bone cancer and stomach cancer and possibly other cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

25 This gene is expressed primarily in epididymus, and lymph node of breast cancer, and to a lesser extent in many other tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, abnormalities of the epididymus, and breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the epididymus and breast, expression of this gene at significantly higher or lower levels may be routinely
35 detected in certain tissues (e.g., epididymus and other reproductive tissue, lymphoid tissue, and mammary tissue, and cancerous and wounded tissues) or bodily fluids

(e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:185 as residues: Arg-57 to Ser-65.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of abnormalities of the epididymus, and breast cancer.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 62

The translation product of this gene appears to be the human homolog of bovine NADH dehydrogenase which is thought to be important in cellular metabolism. In specific embodiments, the polypeptides of the invention comprise the amino acid sequence: SMSALTRLASFARVGGRLFRSGCARTAGDGGVRHAGGGVHIEPRY
15 RQFPQLTRSQVFQSEFFSGLMFWILWRFWHDSEEVLGHFPYPDPSQWTDEEL
GIPDDED (SEQ ID NO:323), or fragments thereof. Polynucleotides encoding this polypeptide are also encompassed by the invention.

This gene is expressed in larynx tumor, lymph node, brain amygdala, human cardiomyopathy, and retina.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases affecting cellular metabolism. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
25 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., larynx, lymphoid tissue, brain and other tissue of the nervous system, heart and cardiovascular tissue, and retina, and cancerous and wounded tissues) or
30 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:208 as residues: Pro-27 to Gln-32, Arg-
35 42 to Glu-51.

The tissue distribution and homology to NADH dehydrogenase indicates that

polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases involving cellular metabolism.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

5 This gene is expressed primarily in amygdala, and to a lesser extent in many other tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
10 not limited to, abnormalities of the amygdala. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the amygdala, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g.,
15 amygdala, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
20 sequence shown in SEQ ID NO:187 as residues: Gln-17 to Glu-29, Pro-41 to Phe-46, Ser-59 to Ile-70, Thr-97 to Leu-105.

 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of abnormalities of
25 amygdala.

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

 This gene is expressed primarily in female bladder, and to a lesser extent in chronic synovitis and hemangiopericytoma.

 Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, bladder cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
35 particularly of the urinary tract, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., bladder, synovial tissue, and

vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:188 as residues: Pro-2 to Gln-7, Pro-27 to Phe-34.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatments of defects of the urinary tract, especially bladder cancer.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in fetal spleen, and to a lesser extent in hemangiopericytoma, thymus, and synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, defects of immune or hematopoietic systems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., spleen, vascular tissue, thymus, blood cells, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The protein product of this gene is useful for treatment of defects of the immune or hematopoietic systems, because of the gene's expression in thymus and spleen.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This gene is expressed primarily in human pituitary and to a lesser extent in placenta and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are

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not limited to, endocrine growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., 5 pituitary and other endocrine tissue, placenta, and pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include 10 those comprising a sequence shown in SEQ ID NO:190 as residues: Val-38 to Asn-44, Gly-53 to Ser-65.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of growth disorders related to 15 pituitary dysfunction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

The translation product of this gene shares sequence homology with a *Caenorhabditis elegans* gene of unknown function. In specific embodiments, the 20 polypeptides of the invention comprise the sequence: DPRRPNKVLRYPKPPSE CNPALDDPTP (SEQ ID NO:317); DYMNLLGMIFSMCGLMLKLKWCAWVA VYCS (SEQ ID NO:318); FISFANSRSEDTKQMMSSF (SEQ ID NO:316); and/or MLSISAVVMSYLQNPQPMTPPW (SEQ ID NO:319). Polynucleotides encoding these polypeptides are also encompassed by the invention.

25 This gene is expressed primarily in primary breast cancer and lymph node breast cancer and to a lesser extent in adult brain, lung cancer, colon cancer, epithelioid sarcoma, and Caco-2 cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a 30 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer and tumor tissues, expression of this gene at significantly 35 higher or lower levels may be routinely detected in certain tissues (e.g., mammary tissue, lymphoid tissue, brain and other tissue of the nervous system, lung, colon, and

epithelium, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:191 as residues: Asn-34 to Lys-42.

The tissue distribution in a variety of cancer tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of a variety of cancer and tumor types.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 68

The translation product of this gene shares sequence homology with steroid membrane binding protein. The translation product of this gene has recently been published as progesterone binding protein. See Genbank AJ002030. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: AAGDGDVKGTLGSGSESSNDGGSESPGDAGAAAXGGGWAAAALALLTG GGE (SEQ ID NO:320).

This gene is expressed primarily in breast, and to a lesser extent in placenta and fetal tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, breast cancer or developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of breast or fetal tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., mammary tissue, placenta, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:192 as residues: Pro-43 to Asp-49, Gln-54 to Pro-64, Asp-110 to Asp-118, Lys-138 to Tyr-143, Pro-150 to Asp-170.

The tissue distribution and homology to steroid membrane binding protein and to progesterone binding protein indicates that the protein products of this gene are

useful for treatment of breast cancers, especially those caused by estrogen and progesterone binding.

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

5 Preferred polypeptides encoded by this gene comprise the following amino acid sequence: AADNYGIPRACRNSARSYGAAWLLXPAGSSRVEPTQDISISDQLGG QDVPVFRNLSLLVVGVGAVFSLLFHLGTRERRRRPHAXEPGEHTPLLAPATAQPL LLWKHWLREXAFYQVGILYMTTRLIVNLSQTYMAMYLTYSLHLPKKFIATIPLV MYLSGFLSSFLMKPINKCIGRN (SEQ ID NO:321).

10 This gene is expressed primarily in macrophage (GM-CSF treated), and to a lesser extent in monocytes and dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and infection. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., macrophages and other blood cells, and dendritic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution indicates that the protein products of this gene are useful for treatment of infection or inflammation or other events or defects involving the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 70

30 This gene is expressed primarily in adult brain and to a lesser extent in thyroid, 12 week old early stage human, and stromal cell TF274.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neurological or neuro-endocrine diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous or endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, 5 thyroid, and stromal cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a 10 sequence shown in SEQ ID NO:194 as residues: Pro-65 to Cys-71.

The tissue distribution indicates that the protein products of this gene are useful for treatment and diagnosis of neurological diseases or metabolic conditions involving the neuro-endocrine system.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 71**

This gene is expressed in T-cell helper and to a lesser extent in adult brain and adult testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a 20 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune disorders, meningitis or reproductive problems. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, neural 25 and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, brain and other tissue of the nervous system, testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual 30 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:195 as residues: Val-18 to Tyr-24, Ala-89 to Asp-99, Asp-104 to Ala-117, Leu-121 to Pro-136.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis immune and

reproductive disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 72

5 The translated polypeptide of this contig has a high degree of identity with the Ob Receptor-Associated Protein deposited as GenBank Accession No. 2266638. No function has been determined for the Ob Receptor-Associated Protein, however it is expressed upon stimulation of the Ob Receptor by Leptin.

This gene is expressed in T-cells and to a lesser extent in endothelial and bone marrow cells.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, acute lymphoblastic leukemia, hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, endothelial cells, and bone marrow, and cancerous and wounded tissues) or
20 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:196 as residues: Ser-61 to Trp-70.

25 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of leukemia and other disorders of the primary immune system. In addition, since this gene appears to be related to the Ob Receptor-Related Protein, it is likely that this polypeptide is also involved in the Ob/Leptin signal transduction cascade. As a result, this protein may be
30 of use in the molecular diagnosis and therapeutic intervention of obesity and related disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 73

35 The translation product of this contig has homology with furin, a protein thought to be a key endopeptidase in the constitutive secretory pathway. The identification and initial characterization of Furin was reported by Takahasi and

colleagues (Biochem Biophys Res Commun 1993 Sep 15;195(2):1019-1026).

This gene is expressed in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases of the immune system such as allergies, wound healing and antigen recognition. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., neutrophils and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of allergies or other immune disorders since neutrophils are an important part of an allergic response. Further, since this protein appears to be related to Furin, it can be used diagnostically and therapeutically to treat secretory protein processing disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

This gene is expressed in the frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, of the motor activity and sensory functions that involve the central nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of neural disorders that affect cognitive functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 75

The translation product of this gene shares sequence homology with inorganic pyrophosphatase which is thought to be important in the catalysis the hydrolysis of diphosphate bonds, chiefly in nucleoside di- and triphosphates and essential enzymes that are important for controlling the cellular levels of inorganic pyrophosphate (PPi). The bovine homolog of this gene has been identified by Yang and Wensel (J. Biol. Chem. 267:24641-24647 (1992)).

This gene is expressed in osteoclastoma cells and to a lesser extent in epithelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoporosis and other bone weakening diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, and epithelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:199 as residues: Lys-22 to Tyr-28, Asp-64 to Lys-77, Pro-86 to Ile-91, Gln-99 to Pro-119, Tyr-169 to Asp-174, Lys-176 to Gly-181, Trp-189 to Asn-202, Lys-233 to Gly-239, Ser-250 to Asp-257.

The tissue distribution and homology to inorganic pyrophosphatase indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of osteoporosis through the removal of bone by demineralization.

FEATURES OF PROTEIN ENCODED BY GENE NO: 76

The translation product of this gene shares exact sequence homology with ATP sulfurylase/APS kinase (GenBank Accession No. 2673862) which is thought to be important in biosynthesis of the activated sulfate donor, adenosine 3'-phosphate 5'-phosphosulfate, involves the sequential action of two enzyme activities: ATP sulfurylase, which catalyzes the formation of adenosine 5'-phosphosulfate (APS) from ATP and free sulfate, and APS kinase, which subsequently phosphorylates APS to produce adenosine 3'-phosphate 5'-phosphosulfate.

This gene is expressed in osteoclastoma cells and to a lesser extent in developmental tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, antibiotic resistant bacterial infections, osteoarthritis and other autoimmune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or skeletal structure expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., bone, and developmental tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:200 as residues: Asn-15 to Trp-20, Ser-36 to Gly-41, Pro-103 to Val-110, Pro-134 to Arg-143, Leu-173 to Arg-178, Ser-190 to Ala-197, His-314 to Arg-319, Arg-354 to Asn-362, Asp-391 to Arg-397, Glu-402 to Asp-409, Asp-434 to Leu-439, Glu-441 to Arg-446, Gly-455 to Asp-462, Pro-528 to His-541, Asn-566 to Arg-571, Tyr-574 to Glu-581, Thr-589 to Glu-603.

The tissue distribution and homology to ATP sulfurylase/APS kinase indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment or detection of autoimmune diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 77

This polypeptide is identical to the SLP-76-associated protein reported by Musci and colleagues (J. Biol. Chem. 272 (18), 11674-11677 (1997)) and to the FYB protein

reported by da Silva and coworkers (Proc. Natl. Acad. Sci. U.S.A. (1997) In press).

These proteins have been reported to be novel T-cell Proteins which bind FYN and SLP-76 and regulate IL-2 production. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: RITDNPEGKWLGRARGSYGYIK

5 TTAVEIXYDSLKLKKDSLGLAPSRPIEDDQEVYDDVAEQDDISSHSQSGSGGIFPP
PPDDDIYDGIEEDADDGFPAPPKQLDMGDEVYDDVDTSDFPVSSAEMSQGTNV
GKAKTEEKDLKKLKKQXKEXKDFRKKFKYDGEIRVLYSTKVTTSITSKKWGT
RDLQVKPGESLEVIQTDDTKVLCRNEEGKYGYVLRSYLADNDGEIYDDIADGC
IYDND (SEQ ID NO:322).

10 This gene is expressed in CD34 positive cells (hematopoietic progenitor cells) and to a lesser extent in adult spleen derived from a chronic lymphocytic leukemia patient.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, chronic lymphocytic leukemia; hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and
20 hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., T-cells and other blood cells, bone marrow, hematopoietic cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
25 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Further, nucleic acids and polypeptides of the present invention are useful both diagnostically and therapeutically in the intervention of immune and other disorders in which the ability to alter IL-2 expression is desired. Preferred epitopes include those comprising a sequence shown in
30 SEQ ID NO:201 as residues: Ala-17 to Lys-37, Val-39 to Ser-45, Lys-59 to His-70, Arg-90 to Leu-95, Lys-97 to Lys-107, Ser-117 to Leu-124, Phe-133 to Ser-138, Trp-146 to Leu-167, Pro-175 to Asn-185, Lys-190 to Ser-211, Pro-213 to Ser-222, His-230 to Pro-235, Pro-240 to Pro-246, Pro-253 to Gly-261, Leu-271 to Leu-303, Leu-305 to Leu-326, Lys-343 to Leu-349, Thr-363 to Leu-371, Arg-373 to Tyr-381, Tyr-391 to Leu-401, Pro-404 to Val-414, Ser-426 to Ser-432, Ile-448 to Ser-457, Gln-462
35 to Trp-468, Lys-477 to Ser-501, Asp-518 to Ser-523, Ala-541 to Gln-554.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of a variety of hematopoietic disorders. The noted expression of this gene in the hematopoietic progenitor cell compartment - as determined by its expression on CD34 positive hematopoietic stem and progenitor cells - indicates that it plays a critical role in the expansion or proliferation of hematopoietic stem/progenitor cells, as well as in the differentiation of the various blood cell lineages. Thus it could be useful in the reconstitution of the hematopoietic system of patients with leukemias and other hematopoietic diseases.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 78**

This gene is homologous to heparin cofactor II (HCII) which is a 66-kDa plasma glycoprotein that inhibits thrombin rapidly in the presence of dermatan sulfate or heparin.

This gene is expressed in apoptotic and anergic T-cells.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, thrombopenia T-cell lymphomas; Hodgkin's lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system - most notably the T-cell compartment, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The homology to heparin cofactor II (HCII) and the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic disorders particularly in thrombopoiesis, most notably of the T-cell compartment. This could include immune modulation, inflammation, immune surveillance, graft rejection, and autoimmunity.

35 **FEATURES OF PROTEIN ENCODED BY GENE NO: 79**

The translation product of this gene shares sequence homology with a mouse

protein believed to represent an integral membrane protein.

This gene is expressed in fetal cochlea and epididymus and to a lesser extent in adult spleen and osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoclastoma; disorders of the inner ear; male fertility disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell
10 type(s). For a number of disorders of the above tissues or cells, particularly of the inner ear; male reproductive tract; bone; and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues (e.g., cochlea, epididymus and other reproductive tissue, spleen, and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
15 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:203 as residues: Lys-13 to Gly-23, Cys-38 to Asp-43, Gly-48 to Trp-53, Cys-223 to Ile-237, Ile-240 to
20 Ser-246.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of hearing and fertility disorders. Likewise, it may have a role in the modulation of immune function and in the treatment of osteoporosis.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 80

The translation product of this gene shares sequence homology with reticulocalbin which is thought to be important in the binding of calcium, particularly within the endoplasmic reticulum.

30 This gene is expressed in endothelial cells and stromal cells and to a lesser extent in osteoblasts, osteoclasts, and T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
35 not limited to, osteoporosis; osteoclastomas; T-cell lymphomas; Hodgkin's disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in

providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculature, bone, and immune systems - particularly the T-cell compartments, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, stromal cells, bone, T-cells and other blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:204 as residues: Lys-20 to Arg-27, Pro-32 to Asp-48, Leu-64 to Arg-72, Asp-108 to Lys-114, Glu-128 to Thr-133, Asp-139 to Phe-147, Thr-196 to Ala-204, Tyr-218 to Glu-228, Val-230 to Gln-236, Arg-241 to Lys-255, Glu-276 to Lys-287.

The tissue distribution and homology to reticulocalbin indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of bone disorders such as osteoporosis; the diagnosis and treatment of T-cell lymphomas and Hodgkin's lymphoma; and the treatment of diseases and defects of the vasculature, such as vascular leak syndrome and aberrant angiogenesis that accompanies tumor growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

The translation product of this gene shares sequence homology with a family of peptide transport genes - particularly the AtPTR2-B gene from *Arabidopsis* - which are thought to be important in the uptake of small peptides.

This gene is expressed in a number of fetal tissues, most notably lung, brain, cochlea, and liver/spleen, and to a lesser extent in osteoclastoma and endometrial tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, osteoclastoma; endometrial tumors; cancer; leukemias. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone and endometrium, expression of this gene at significantly higher or lower levels may be

5 routinely detected in certain tissues (e.g., fetal tissue, pulmonary tissue, bone, brain and other tissue of the nervous system, cochlea, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:205 as residues: Lys-186 to Asn-199, Pro-202 to Ala-207.

10 The tissue distribution and homology to peptide transport genes indicates that polynucleotides and polypeptides corresponding to this gene are useful for the control of cell proliferation, owing to its strong expression in fetal tissues undergoing active cell division, as well as its expression in a variety of tumors or cancers of adult tissues. Potentially, it may regulate the uptake of peptides that stimulate cell proliferation. This gene product may also be useful in stimulating the uptake of a variety of peptide-based
15 drug compounds.

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

This gene is expressed in fetal liver and spleen and to a lesser extent in endothelial cells.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cancer and tumors of a hematopoietic and/or endothelial cell origin; leukemias. Similarly, polypeptides and antibodies directed to these polypeptides are
25 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and/or vasculature, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, endothelial cells, vascular tissue, and tissue and cells of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine,
30 synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
35 NO:206 as residues: Met-1 to Asp-9, Arg-66 to Gly-76, Asp-164 to Arg-171.

The tissue distribution indicates that polynucleotides and polypeptides

corresponding to this gene are useful for the treatment of disorders of the immune system. Expression of this gene product in both fetal liver/spleen and endothelial cells indicates that it may be expressed in the hemangioblast, the progenitor cell for both the immune system and the vasculature. Thus, it is most likely expressed in hematopoietic stem cells, and may be useful for the expansion of hematopoietic stem and progenitor cells in conjunction with cancer treatment for a variety of leukemias.

FEATURES OF PROTEIN ENCODED BY GENE NO: 84

The translation product of this gene shares sequence homology with NADH dehydrogenase which is thought to be important in cellular metabolism.

This gene is expressed in fetal dura mater and to a lesser extent in T-cells and hypothalamus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, diseases affecting cellular metabolism. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, T-cells and other blood cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:208 as residues: Pro-27 to Gln-32, Arg-42 to Glu-51.

The tissue distribution and homology to NADH dehydrogenase indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases involving cellular metabolism.

FEATURES OF PROTEIN ENCODED BY GENE NO: 85

The translation product of this gene shares sequence homology with I-TRAF, a novel TNF receptor associated factor (TRAF)-interacting protein that regulates TNF receptor-mediated signal transduction. This protein is thought to be important in
5 regulating the cellular response to tumor necrosis factor (TNF), which is an important mediator of inflammation.

This gene is expressed in endothelial cells and to a lesser extent in glioblastoma and osteoblastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation; glioblastoma and osteoblastoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of
15 disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, bone, and glial cells and tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
20 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:209 as residues: Glu-15 to Thr-22, Glu-46 to Leu-62, Arg-103 to Glu-119, Gln-127 to Glu-132, Asn-152 to Trp-158, Gln-191 to Gln-210, Glu-264 to Thr-271, Tyr-
25 282 to Leu-288, Trp-319 to Thr-331, Glu-335 to Ser-348, Ser-353 to Ser-358, Asp-382 to Asn-392.

The tissue distribution and homology to I-TRAF indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammatory diseases, including rheumatoid arthritis, sepsis, inflammatory bowel
30 disease, and psoriasis, particularly where tumor necrosis factor is known to be involved.

FEATURES OF PROTEIN ENCODED BY GENE NO: 86

This gene has homology with a candidate gene involved in X-linked Retinopathy reported by Wong and colleagues (Genomics 15:467-471 (1993)).

This gene is expressed in a T-cell line.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, inflammation and autoimmune diseases; T-cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
10 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., T-cells and other blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
15 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammatory
20 disorders such as sepsis, inflammatory bowel disease, psoriasis, and rheumatoid arthritis as well as autoimmune disease such as lupus. It could also be useful in immune modulation and in the process of immune surveillance. The present invention can be used diagnostically and therapeutically to treat X-linked Retinopathy.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 87

This gene is expressed in human brain tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are
30 not limited to, brain disorders; neurodegenerative disorders; tumors of a brain origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels
35 may be routinely detected in certain tissues (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID

5 NO:211 as residues: Cys-32 to Tyr-38.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of CNS disorders such as epilepsy, paranoia, depression, Alzheimer's disease, and schizophrenia. It could be useful in the survival and/or proliferation of neurons and could effect neuronal
10 regeneration.

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
1	HAGEW82	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	11	1679	247	1607	353	353	125	1			30
2	HAGFY16	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	12	1830	87	1786	128	128	126	1	26	27	44
2	HBMCF37	xxxxx 03/19/98	pBluescript	98	1487	79	1487	170	170	212	1	44	45	69
2	HFLQB16	209641 02/25/98	Uni-ZAP XR	99	1653	394	1637	413	413	213	1	25	26	81
3	HALAA60	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	13	1212	1	1212	99	99	127	1	24	25	38
4	HAPBL78	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	14	2061	882	2061	900	900	128	1	22	23	22
5	HASAV70	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	15	1412	10	733	103	103	129	1	20	21	109

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
6	HBNAF22	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	16	1052	276	880	538	538	130	1	17	18	62
7	HBNBL77	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	17	683	1	683	181	181	131	1			29
8	HCDDR90	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	18	1054	86	1007	86	86	132	1	23	24	52
9	HCEEF50	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	19	1393	132	1393	192	192	133	1	17	18	56
10	HCEMU42	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	20	1215	277	1070	401	401	134	1	18	19	215
11	HCENE16	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	21	2042	614	2011	793	793	135	1	26	27	48

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
12	HMSJJ74	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	22	1872	21	1872	69	69	136	1	23	24	67
13	HCUBF15	97923 03/07/97 209071 05/22/97	ZAP Express	23	289	1	289	89	89	137	1	29	30	51
14	HE2DE47	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	24	3533	2821	3532	808	808	138	1	30	31	539
14	HE2DE47	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	100	1145	435	1115	515	515	214	1	22	23	80
15	HKMLH01	209179 07/24/97	pBluescript	25	1148	171	907	196	196	139	1	26	27	56
15	HE6DG34	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	101	734	25	734	295	295	215	1	36	37	48
16	HE9DG49	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	26	717	1	717	70	70	140	1	27	28	200

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
16	HE9DG49	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	102	713	17	713	78	78	216	1	28	29	202
17	HELBA06	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	27	1099	1	1099	38	38	141	1	22	23	215
17	HELBA06	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	103	1080	1	1080	149	149	217	1	25	26	185
18	HSLFM29	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	28	941	171	941	128	128	142	1	42	43	101
19	HELBW38	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	29	756	62	756	294	294	143	1	30	31	111
20	HETHN28	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	30	2100	408	2093	496	496	144	1			19

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
21	HFC DK17	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	31	1448	475	1392	567	567	145	1			29
22	HFEAF41	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	32	456	1	409	21	21	146	1	28	29	98
23	HFKFL13	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	33	1326	1	1322	210	210	147	1			7
24	HFSBG13	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	34	710	1	710	242	242	148	1	16	17	38
25	HFTBE43	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	35	1188	110	1161	178	178	149	1	26	27	130
26	HFTDJ36	97923 03/07/97 209071 05/22/97	Uni-ZAP XR	36	956	1	938	144	144	150	1	21	22	31
27	HKTAC77	97924 03/07/97	Uni-ZAP XR	37	1603	974	1581	1104	1104	151	1			13

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
28	HLHSH36	97924 03/07/97	pBluescript	38	1089	55	1067		209	152	1			7
29	HLHSV96	97924 03/07/97	pBluescript	39	629	1	629	119	119	153	1	32	33	67
30	HLQBQ86	97924 03/07/97	Lambda ZAP II	40	1964	408	1793	581	581	154	1			25
31	HLTBX31	97924 03/07/97	Uni-ZAP XR	41	1522	13	1123	126	126	155	1	32	33	194
32	HLTCJ63	97924 03/07/97	Uni-ZAP XR	42	875	1	875	43	43	156	1	18	19	90
33	HMKAH44	97924 03/07/97	pSport1	43	843	1	843	171	171	157	1	30	31	30
34	HMQAJ64	97924 03/07/97	Uni-ZAP XR	44	489	3	489	55	55	158	1	19	20	89
34	HMQAJ64	97924 03/07/97	Uni-ZAP XR	104	489	6	489	58	58	218	1	22	23	89
35	HOABG65	97924 03/07/97	Uni-ZAP XR	45	534	1	534	17	17	159	1	18	19	88
36	HODCL36	97924 03/07/97	Uni-ZAP XR	46	1374	1	1374	15	15	160	1	20	21	173
36	HODCL36	97924 03/07/97	Uni-ZAP XR	105	640	58	640	72	72	219	1	20	21	137
36	HODCL36	97924 03/07/97	Uni-ZAP XR	106	1529	40	1399	54	54	220	1	27	28	47
37	HODCL50	97924 03/07/97	Uni-ZAP XR	47	596	1	596	269	269	161	1	27	28	44

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
38	HODCV74	97924 03/07/97	Uni-ZAP XR	48	851	99	822	170	162	1			22
39	HODCZ16	97924 03/07/97	Uni-ZAP XR	49	2020	569	2020	638	163	1	17	18	69
40	HTOEU03	97924 03/07/97	Uni-ZAP XR	50	2432	848	2432	99	164	1	19	20	322
40	HTOEU03	97924 03/07/97	Uni-ZAP XR	107	2435	849	2435	928	221	1	31	32	69
41	HPBCJ74	97924 03/07/97	pBluescript SK-	51	2340	1627	2340	150	165	1	60	61	319
41	HPBCJ74	97924 03/07/97	pBluescript SK-	108	805	92	791	239	222	1	21	22	82
42	HPMBU33	97924 03/07/97	Uni-ZAP XR	52	601	188	601	432	166	1			30
43	HSAUL66	97924 03/07/97	Uni-ZAP XR	53	359	1	337	142	167	1	18	19	71
44	HSIDQ18	97924 03/07/97	Uni-ZAP XR	54	1141	1	1141	25	168	1	30	31	280
44	HSIDQ18	97924 03/07/97	Uni-ZAP XR	109	1166	21	1166	433	223	1	30	31	42
45	HSJBB37	97924 03/07/97	Uni-ZAP XR	55	1560	63	1148	217	169	1			22
46	HSJBQ79	97924 03/07/97	Uni-ZAP XR	56	1507	164	608	57	170	1	19	20	326
46	HSJBQ79	97924 03/07/97	Uni-ZAP XR	110	586	4	586	35	224	1	23	24	183

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
47	HTEGA76	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	57	450	1	450	83	83	171	1	35	36	68
48	HTEJN13	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	58	1147	1	1147	163	163	172	1	15	16	158
48	HTEJN13	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	111	1134	1	1134	155	155	225	1	19	20	70
49	HTHBL86	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	59	777	1	777	115	115	173	1	18	19	122
50	HTSFO71	97958 03/13/97 209072 05/22/97	pBluescript	60	1191	48	598	52	52	174	1	30	31	128
50	HTSFO71	97958 03/13/97 209072 05/22/97	pBluescript	112	1333	594	1333	829	829	226	1			9
51	HAPNO80	209235 09/04/97	Uni-ZAP XR	61	1580	443	1554	114	114	175	1	1	2	371

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
51	HAUCC47	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	113	1015	249	708	244	244	227	1	28	29	137
52	HBMCL41	97958 03/13/97 209072 05/22/97	pBluescript	62	1117	105	1034	182	182	176	1	28	29	215
53	HCFLD84	97958 03/13/97 209072 05/22/97	pSport1	63	361	1	361	97	97	177	1	32	33	54
54	HE8EM69	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	64	1668	1	1638	150	150	178	1	20	21	22
55	HE8EZ48	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	65	1353	35	1303	231	231	179	1	33	34	102
56	HEBGF73	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	66	1011	655	1011	703	703	180	1	38	39	47

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
57	HFEBF41	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	67	1193	267	1090	459	459	181	1	35	36	95
58	HFRBU14	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	68	560	1	560	63	63	182	1	29	30	94
59	HFVGZ79	97958 03/13/97 209072 05/22/97	pBluescript	69	1657	765	1581	839	839	183	1	21	22	26
60	HHGCM76	97958 03/13/97 209072 05/22/97	Lambda ZAP II	70	711	8	711	270	270	184	1			10
61	HHGCO88	97958 03/13/97 209072 05/22/97	Lambda ZAP II	71	935	111	935	272	272	185	1	19	20	64
62	HHGCP52	97958 03/13/97 209072 05/22/97	Lambda ZAP II	72	504	113	484	127	127	186	1	21	22	21

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
63	HHGDB72	97958 03/13/97 209072 05/22/97	Lambda ZAP II	73	620	1	620	96	96	187	1	18	19	131
64	HHGDI71	97958 03/13/97 209072 05/22/97	Lambda ZAP II	74	581	156	581	248	248	188	1	32	33	68
65	HHSDI45	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	75	1843	537	1786	630	630	189	1	27	28	44
66	HHSEB66	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	76	1441	116	800	167	167	190	1	36	37	64
67	HJPAZ83	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	114	1076	398	1076		575	228	1	11	12	22
68	HLDBO49	97958 03/13/97 209072 05/22/97	pCMVSPORT 3.0	78	2776	18	1888	187	187	192	1	14	15	169

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
69	HLDBQ19	97958 03/13/97 209072 05/22/97	pCMVSPORT 3.0	79	1525	401	1480	534	534	193	1	22	23	65
69	HLDBQ19	209226 08/28/97	pCMVSPORT 3.0	115	1487	401	1487	534	534	229	1	22	23	131
70	HMSGT42	97958 03/13/97 209072 05/22/97	Uni-ZAP XR	80	1563	33	1077	40	40	194	1	32	33	91
71	HMWIC78	97957 03/13/97 209073 05/22/97	Uni-Zap XR	81	1020	18	780	238	238	195	1	23	24	175
72	HTTCT79	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	82	770	101	770	286	286	196	1	26	27	69
73	HNGJU84	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	83	481	1	481	58	58	197	1	20	21	24
74	HNTAC73	97957 03/13/97 209073 05/22/97	pCMVSPORT 3.0	84	644	1	623	14	14	198	1	25	26	72

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
75	HOSEI45	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	85	1351	435	1284	98	98	199	1	12	13	288
75	HOSEI45	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	116	1350	428	1283		545	230	1			27
76	HOSFD58	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	86	2527	290	1747	56	56	200	1	30	31	623
76	HOSFD58	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	117	2527	288	1747	477	477	231	1	32	33	60
77	HSAUM95	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	87	2566	1843	2566	251	251	201	1	30	31	648
77	HSAUM95	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	118	1098	375	1098	677	677	232	1	21	22	28

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
78	HSAUR67	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	88	540	1	540	83	83	202	1	32	33	54
79	HSKDI81	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	89	1863	152	1165	188	188	203	1	11	12	265
79	HSKDI81	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	119	1679	152	1166	315	315	233	1			17
80	HSKDW91	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	90	2478	1149	2449	92	92	204	1	19	20	314
81	HTLEX50	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	91	2058	476	2058	414	414	205	1	20	21	206
82	HSKHL65	97957 03/13/97 209073 05/22/97	pBluescript	92	1411	345	1411	157	157	206	1	69	70	194

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
82	HSKHL65	97957 03/13/97 209073 05/22/97	pBluescript	121	1411	345	1411	526	526	235	1	37	38	71
83	HHFGA11	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	93	2187	147	2184	397	397	207	1	30	31	329
83	HHFGA11	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	122	2256	138	2063	228	228	236	1	19	20	95
84	HWTBL40	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	94	757	524	608	445	445	208	1	20	21	57
85	HBXFG80	97957 03/13/97 209073 05/22/97	ZAP Express	95	2394	481	2394	523	523	209	1	1	2	391
86	HCACY32	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	96	672	1	672	117	117	210	1	21	22	25

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Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
87	HCEDO21	97957 03/13/97 209073 05/22/97	Uni-ZAP XR	97	1419	1	1419	207	207	211	1	20	21	37

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

5 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources
10 using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

Methods for predicting whether a protein has a signal sequence, as well as the
15 cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1
20 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra*.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide
25 was analyzed by a computer program called SignalP (Henrik Nielsen et al., *Protein Engineering* 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results
30 shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., +
35 or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Polynucleotide and Polypeptide Variants

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization

Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query

amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions,

- 5 interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be
10 determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and
15 subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window
20 Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity.
25 For subject sequences truncated at the N- and C-termini, relative to the the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of
30 the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are
35 considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired
5 residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence.
10 This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query
15 sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or
20 activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in
25 the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level.
30 Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be
35 deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., *J. Biol. Chem.* 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after

deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about
5 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers
10 as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide
15 number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, or 701 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the
25 invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1)
30 amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-
35 60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any

combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et

al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However,

- 5 immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

- As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')₂ fragments) which are capable of specifically binding to protein. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library.
- 15 Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

- Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.
- 25

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

- Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.
- 30
- 35

Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example
5 describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the
10 monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a
15 fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for
20 example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker
25 sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for
30 instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral
5 vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is
10 a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to
15 name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or
20 UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of
25 appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1
35 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods
5 In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography,
10 phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also
15 be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production
20 procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein
25 after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

30 **Uses of the Polynucleotides**

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The polynucleotides of the present invention are useful for chromosome
35 identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat

polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be
5 selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the
10 polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome
15 specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al.,
20 "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides
25 correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage
30 analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease
35 could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined.

First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying

personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

5 The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set
10 of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

 Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as
15 tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more
20 restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

 There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of
25 unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

30 In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using
35 DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

5 A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay
10 (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

15 In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for
20 NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, 131I,
25 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human
30 subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of 99mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The
35 Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the

proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders
5 may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in
10 treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to:
15 blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also
20 be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet
25 disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in
30 treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the
35 present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect

interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes

Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus, Haemophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, 5 Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide 10 of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide 15 of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

20 A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal 25 disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and 30 skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or 35 polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue

regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate
5 nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized
10 neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

15 **Chemotaxis**

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of
20 hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system
25 disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present
30 invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

35 A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying
5 agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

10 A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color,
15 skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change
20 a mammal's mental state or physical state by influencing biorhythms, circadian rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

25 A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

35 Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of

positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous
5 nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of
10 contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide
15 sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide
20 sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a
nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ
ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the
First Amino Acid of the Signal Peptide and ending with the nucleotide at about the
25 position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in
Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising
a nucleotide sequence which is at least 95% identical to the complete nucleotide
sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under
30 stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which
35 comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type

Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous
5 nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete
10 open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising
15 a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

20 A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone
25 identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95%
30 identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of
35 comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino
5 acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at
10 least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence
15 at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone
20 identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and
25 contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA
30 clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA
35 clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide
5 comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

10 Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

15 Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid
20 sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human
25 cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an
30 individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of
35 illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

5 Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For
10 example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
15	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
20	pCR [®] 2.1	pCR [®] 2.1

 Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Altting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Altting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are
25 commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer
30 sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

35 Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain

DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., *Focus* 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. et al., *Bio/Technology* 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl₂, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is

used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

5

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X.,
10 according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by,
15 among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is
20 then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are
25 mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5'
30 end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual
35 chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on

either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

5 **Example 5: Bacterial Expression of a Polypeptide**

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as
10 BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site
15 (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses
20 the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml).
25 The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

30 Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from
35 QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high

affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed
5 with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The
10 recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer
15 plus 200 mM NaCl. The purified protein is stored at 4° C or frozen at -80° C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a
20 neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (*lacIq*). The origin of replication (*oriC*) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR
25 primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible
30 enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

- 5 Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50
10 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

- The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by
15 centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

- The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C
20 overnight to allow further GuHCl extraction.

- Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing
25 for 12 hours prior to further purification steps.

- To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive
30 Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μ g of a plasmid containing the polynucleotide is co-transfected with 1.0 μ g of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One μ g of BaculoGold™ virus DNA and 5 μ g of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μ l of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μ l Lipofectin plus 90 μ l Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life

Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.)

5 After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μ l of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested
10 and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is
15 removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 μ Ci of 35 S-methionine and 5 μ Ci 35 S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE
20 followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell.
25 A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved
30 with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden),
35 pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used

include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No.209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

5 The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for
10 transfection. Five μ g of the expression plasmid pC6 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are
15 trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of
20 methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

25

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose
30 binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the
35 activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion

proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

5 Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

10 For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

15 If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

20 Human IgG Fc region:

GGGATCCGGAGCCCAAATCTTCTGACAAACTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAACC
CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
25 GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT
30 GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA
GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
35 GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide.

Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in

5 Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of

10 transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off

15 PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl₂ (anhyd); 0.00130 mg/L

20 CuSO₄·5H₂O; 0.050 mg/L of Fe(NO₃)₃·9H₂O; 0.417 mg/L of FeSO₄·7H₂O; 311.80 mg/L of KCl; 28.64 mg/L of MgCl₂; 48.84 mg/L of MgSO₄; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO₃; 62.50 mg/L of NaH₂PO₄·H₂O; 71.02 mg/L of Na₂HPO₄; .4320 mg/L of ZnSO₄·7H₂O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic

25 Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitic Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H₂O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H₂O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0

30 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H₂O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22

35 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H₂O; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of

Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 5 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x 10 penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B 15 adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

20 It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an 25 activity in a particular assay.

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs 30 pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six 35 members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in

many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

5 The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

10 The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and
15 (b) Class 2 includes IFN- α , IFN- γ , and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

20 Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

 Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are
25 known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>Ligand</u>	<u>tyk2</u>	<u>JAKs</u> <u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>	<u>STATS</u>	<u>GAS(elements) or ISRE</u>
5	<u>IFN family</u>						
	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS (IRF1>Lys6>IFP)
	Il-10	+	?	?	-	1,3	
10	<u>gp130 family</u>						
	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS (IRF1>Lys6>IFP)
	Il-11(Pleiotrohic)	?	+	?	?	1,3	
	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
15	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
20	<u>g-C family</u>						
	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
25	<u>gp140 family</u>						
	IL-3 (myeloid)	-	-	+	-	5	GAS (IRF1>IFP>>Ly6)
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
30	<u>Growth hormone family</u>						
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	GAS(B-CAS>IRF1=IFP>>Ly6)
35	<u>Receptor Tyrosine Kinases</u>						
	EGF	?	+	+	-	1,3	GAS (IRF1)
	PDGF	?	+	+	-	1,3	
40	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5':GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCG
AAATGATTTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5':CTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAATG
ATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
CTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGC
CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGC
CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT
TGCAAAAAGCTT:3' (SEQ ID NO:5)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

- During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final
5 concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

- 10 On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

- 15 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

- After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12
20 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

- The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples
25 from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

- 30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 10 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 15 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37°C for 45 min.

- 20 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 25 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

- 30 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine

growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating

diseases. For example, inhibitors of NF- κ B could be used to treat those diseases related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC
TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTGGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)

Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGGACTTTCC
ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCCA
TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT
AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTC
CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:
3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 μ l of 2.5x dilution buffer into Optiplates containing 35 μ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 μ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 μ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6

23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

5 For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10⁶ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10⁶ cells/ml, and dispensed into a microplate, 100
10 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the
15 following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca⁺⁺ concentration.

20

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase
25 RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

30 Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members
35 of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a

biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

- 5 The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂₊ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the
- 10 components gently and preincubate the reaction mix at 30°C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

- Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction
- 15 mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as
- 20 above.

- Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of
- 25 tyrosine kinase activity.

Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

- As a potential alternative and/or compliment to the assay of protein tyrosine
- 30 kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,
- 35 Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other

phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies).

The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

5 PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

10 Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenin deoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

15 Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated
25 disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

30 A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

35 For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 µg/kg/hour to about 50 µg/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally,

intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2-hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D-(-)-3-hydroxybutyric acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form.

5 Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

10 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

15 Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 20 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

Example 26: Method of Treatment Using Gene Therapy

25 One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is 30 turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

5 pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

10 The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to
15 transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is
20 then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media,
25 containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is
30 required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

- 5 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.

(1) GENERAL INFORMATION:

- (i) APPLICANT: Human Genome Sciences, Inc. et al.
(ii) TITLE OF INVENTION: 87 Human Secreted Proteins
(iii) NUMBER OF SEQUENCES: 323
(iv) CORRESPONDENCE ADDRESS:

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(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
(B) COMPUTER: HP Vectra 486/33
(C) OPERATING SYSTEM: MSDOS version 6.2
(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
(B) FILING DATE: March 19, 1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: A. Anders Brookes
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PZ004PCT

(vi) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (301) 309-8504
(B) TELEFAX: (301) 309-8439

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

164

GGGATCCGGA GCCCAAATCT TCTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG 60
 AATTTCGAGGG TGCACCGTCA GTCTTCCTCT TCCCCCAAA ACCCAAGGAC ACCCTCATGA 120
 5 TCTCCCGGAC TCCTGAGGTC ACATGCGTGG TGGTGGACGT AAGCCACGAA GACCCTGAGG 180
 TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG 240
 AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT 300
 10 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA ACCCCCATCG 360
 AGAAAACCAT CTCCAAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC 420
 15 CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT 480
 ATCCAAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA GCCGAGAAC AACTACAAGA 540
 CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG 600
 20 ACAAGAGCAG GTGGCAGCAG GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC 660
 ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG TAAATGAGTG CGACGGCCGC 720
 25 GACTCTAGAG GAT 733

30 (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

40 Trp Ser Xaa Trp Ser
 1 5

45 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

55 GCGCCTCGAG ATTTCCCGA AATCTAGATT TCCCCGAAAT GATTTCCCG AAATGATTTT 60
 CCCGAAATAT CTGCCATCTC AATTAG 86

60

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCGGCAAGCT TTTTGCAAAG CCTAGGC 27

15

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTCGAGATTT CCCCAGAAATC TAGATTTCCC CGAAATGATT TCCCCGAAAT GATTTCCCCG 60

AAATATCTGC CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC 120

30 GCCCCTAACT CCGCCAGTT CCGCCATTC TCCGCCCAT GGCTGACTAA TTTTTTTTAT 180

TTATGCAGAG GCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT GAGGAGGCTT 240

35 TTTTGGAGGC CTAGGCTTTT GCAAAAAGCT T 271

40 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

50 GCGCTCGAGG GATGACAGCG ATAGAACCCC GG 32

55 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

5 GCGAAGCTTC GCGACTCCCC GGATCCGCCT C 31

10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

20 GGGGACTTTC CC 12

25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

35 GCGGCCTCGA GGGGACTTTC CCGGGGACTT TCCGGGGACT TTCCGGGACT TTCCATCCTG 60
CCATCTCAAT TAG 73

40

(2) INFORMATION FOR SEQ ID NO: 10:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTCGAGGGGA CTTTCCCGG GACTTTCCGG GGACTTTCCG GGACTTTCCA TCTGCCATCT 60
55 CAATTAGTCA GCAACCATAG TCCCGCCCT AACTCCGCC ATCCCGCCCC TAACTCCGCC 120
CAGTTCGCC CATCTCCGC CCCATGGCTG ACTAATTTT TTTATTTATG CAGAGGCCGA 180
GGCCGCCTCG GCCTCTGAGC TATTCCAGAA GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG 240
60

CTTTTGCAAA AAGCTT

256

5

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1679 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

15

GCAGCGCACC CGGGCGATCG CTTCACGGAT GCGGACGACG TAGCCATCCT TACCTACGTG 60

AAGGAAAATG CCCGCTCGCC CAGCTCCGTC ACCGGTAACG CCTTGTGGAA AGCGATGGAG 120

20

AAGAGCTCGC TCACGCAGCA CTCGTGGCAG TCCCTGAAGG ACCGCTACCT CAAGCACCTG 180

CGGGGCCAGG AGCATAAGTA CCTGCTGGGG GACGCGCCGG TGAGCCCTC CTCCCAGAAG 240

25

CTCAAGCGGA AGGCGGAGGA GGACCCGGAG GCCGCGGATA GCGGGGAACC ACAGAATAAG 300

AGAACTCCAG ATTTGCCTGA AGAAGAGTAT GTGAAGGAAG AAATCCAGGA GAATGAAGAA 360

GCAGTCAAAA AGATGCTTGT GGAAGCCACC CGGGAGTTTG AGGAGGTTGT GGTGGATGAG 420

30

AGCCCTCCTG ATTTTGAAAT ACATATAACT ATGTGTGATG ATGATCCACC CACACCTGAG 480

GAAGACTCAG AAACACAGCC TGATGAGGAG GAAGAAGAAG AAGAAGAAAA AGTTTCTCAA 540

35

CCAGAGGTGG GAGCTGCCAT TAAGATCATT CGGCAGTTAA TGGAGAAGTT TAACTTGGAT 600

CTATCAACAG TTACACAGGC CTTCTTAAAA AATAGTGGTG AGCTGGAGGC TACTTCCGCC 660

TTCTTAGCGT CTGGTCAGAG AGCTGATGGA TATCCCATTT GGTCCCGACA AGATGACATA 720

40

GATTTGCAAA AAGATGATGA GGATACCAGA GAGGCATTGG TCAAAAATTT TGGTGCTCAG 780

AATGTAGCTC GGAGGATTGA ATTTGGAAG AAATAATTGG CAAGATAATG AGAAAAGAAA 840

45

AAAGTCATGG TAGGTGAGGT GGTAAAAAAA AATTGTGACC AATGAACTTT AGAGAGTTCT 900

TGCAATGGAA CTGGCACTTA TTTTCTGACC ATCGCTGCTG TTGCTCTGTG AGTCCTAGAT 960

TTTTGTAGCC AAGCAGAGTT GTAGAGGGGG ATAAAAAGAA AAGAAATTGG ATGTATTTAC 1020

50

AGCTGTCCTT GAACAAGTAT CAATGTGTTT ATGAAAGGAA GATCTAAATC AGACAGGAGT 1080

TGGTCTACAT AGTAGTAATC CATTTGTGGA ATGGAACCCCT TGCTATAGTA GTGACAAAGT 1140

55

GAAAGGAAAT TTAGGAGGCA TAGGCCATTT CAGGCAGCAT AAGTAATCTC CTGTCCTTTG 1200

GCAGAAGCTC CTTTAGATTG GGATAGATTC CAAATAAAGA ATCTAGAAAT AGGAGAAGAT 1260

TTAATTATGA GGCCTTGAAC ACGGATTATC CCCAAACCCCT TGTCAATTTCC CCCAGTGAGC 1320

60

TCTGATTTCT AGACTGCTTT GAAAATGCTG TATTCATTTT GCTAACTTAG TATTTGGGTA 1380

5 CCCTGCTCTT TGGCTGTTCT TTTTTTGGAG CCCTTCTCAG TCAAGTCTGC CGGATGTCTT 1440
 TCTTTACCTA CCCCTCAGTT TTCCTTAAAA CGCGCACACA ACTCTAGAGA GTGTTAAGAA 1500
 TAATGTTACT TGGTTAATGT GTTATTTATT GAGTATTGTT TGTGCTAAGC ATTGTGTTAG 1560
 ATTTAAAAAA TTAGTGGATT GACTCCACTT TGTGTGTGTG TTTTCATTGT TGAAAATAAA 1620
 10 TATAACTTTG TATTCGAAAA AAAAAAAAAA AAAATNRC TG CGNCCGACA AGGGAATTC 1679

15 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1830 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

25 GCGACCGCGC CCTTCAGCTA GCTCGCTCGC TCGCTCTGCT TCCCTGCTGC CGGCTGCGCA 60
 TGGCTTNGGC GTTGGCGGCG CTGGCGGCGG TCGAGCNGCC TGCGSAGCCG GTACCAGCAG 120
 TTGCAGAATG AAGAAGAGTC TGGAGAACCT GAACAGGCTG CAGGTGATGC TCCTCCACCT 180
 30 TACAGCAGCA TTTCTGCAGA GAGCGCACAT NATTTTGA CT ACAAGGATGA GTCTGGGTTT 240
 CCAAAGCCCC CATCTTACAA TGTAGCTACA AACTGCCCA GTTATGATGA AGCGGAGAGG 300
 35 ACCAAGGCTG AAGCTACTAT CCCTTTGGTT CCTGGGAGAG ATGAGGATTT TGTGGGTCGG 360
 GATGATTTTG ATGATGCTGA CCAGCTGAGG ATAGGAAATG ATGGGATTTT CATGTTAACT 420
 TTTTTCATGG CATTCCTCTT TAACTGGATT GGGTTTTTCC TGTCTTTTGG CCTGACCACT 480
 40 TCAGCTGCAG GAAGGTATGG GGCCATTTCA GGATTTGGTC TCTCTCTAAT TAAATGGATC 540
 CTGATTTGTA GGTTTTCCAC CTATTTCCCT GGATATTTTG ATGGTCAGTA CTGGCTCTGG 600
 45 TGGGTGTTCC TTGTTTTAGG CTTTCTCCTG TTTCTCAGAG GATTATCAA TTATGCAAAA 660
 GTTCGGAAGA TGCCAGAAAC TTTCTCAAAT CTCCCCAGGA CCAGAGTTCT CTTTATTTAT 720
 TAAAGATGTT TTCTGGCAA GGCCTTCCTG CATTTATGAA TTCTCTCTCA AGAAGCAAGA 780
 50 GAACACCTGC AGGAAGTGAA TCAAGATGCA GAACACAGAG GAATAATCAC CTGCTTTTAA 840
 AAAATAAAGT ACTGTTGAAA AGATCATTTT TCTCTATTTG TTCCTAGGTG TAAAATTTTA 900
 55 ATAGTTAATG CAGAATTCTG TAATCATTTG ATCATTAGTG GTTAATGTTT GAAAAAGCTC 960
 TTGCAATCAA GTCTGTGATG TATTAATAAT GCCTTATATA TTGTTTGTAG TCATTTTAA 1020
 TAGCATGAGC CATGTCCCTG TAGTCGGTAG GGGGCAGTCT TGCTTTATTTC ATCCTCCATC 1080
 60

169

TCAAAATGAA CTGGGAATTA AATATTGTAA GATATGTATA ATGCTGGCCA TTTTAAAGGG 1140
 GTTTTCTCAA AAGTTAACT TTTGTTATGA CTGTGTTTTT GCACATAATC CATATTTGCT 1200
 5 GTTCAAGTTA ATCTAGAAAT TTATTCAATT CTGTATGAAC ACCTGGAAGC AAAATCATAG 1260
 TGCAAAAATA CATTTAAGGT GTGGTCAAAA ATAAGTCTTT AATTGGTAAA TAATAAGCAT 1320
 10 TAATTTTTTA TAGCCTGTAT TCACAATTCT GCGGTACCTT ATTGTACCTA AGGGATTCTA 1380
 AAGGTGTTGT CACTGTATAA AACAGAAAGC ACTAGGATAC AAATGAAGCT TAATTACTAA 1440
 AATGTAATTC TTGACACTCT TTCTATAATT AGCGTTCCTC ACCCCCACCC CCACCCCCAC 1500
 15 CCCCCTTATT TTCCTTTTGT CTCCTGGTGA TTAGGCCAAA GTCTGGGAGT AAGGAGAGGA 1560
 TTAGGTACTT AGGAGCAAAG AAAGAAGTAG CTTGGAACCTT TTGAGATGAT CCCTAACATA 1620
 CTGTACTACT TGCTTTTACA ATGTGTTAGC AGAAACCACT GGGTTATAAT GTAGAATGAT 1680
 20 GTGCTTTCTG CCCAAGTGGT AATTCATCTT GGTTCGTAT GTTAAACTG TAAATACAAC 1740
 AGAACATTAA TAAATATCTC TTGTGTAGCA CCTTTTAAAA AAAAAAAAAA AAAAAAAAAA 1800
 25 AAAAAAAAAA AANCCCGGGG GGGGGCCCN 1830

30 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

40 TGTTTGAAGT TGTTACTTTT GTTTACAGCA AAGTTTGATG TAGTGTGCAG TAGTGAGCTC 60
 TAGACTGATC TTTTCTAAA TCAGAAAGTG ATTAAAGTAT GCACAACCAA AGGCAGGTTT 120
 TTCTTTTCA TTTATTTCAGC AACTATTTAT TAAGCATCAA CTCTGTGCCA GGCACGTTAC 180
 45 TAGCTGCTAC ATACTGTCTG AACATGACAT ACGGTTAAGT AACTTTACAA TTATTATCAA 240
 ATACTTCAAT GTAGATATTT CTTAAGTTGA AATAGCATTA ACTAGGATAA TGCTTTCATG 300
 50 TTATTTTATT TGTCTGTGA TAGAAATCA ACTTTGTACC ATCTTAAAC TAGGTTGCTA 360
 TAAAAATAGG AGGATGAAGT CAATAAAGTT TATGCCAGTT TAAAACTGG AAGGAAAAGG 420
 TAAGAGCTCT CCATTATAAA ATAGTTGCAT TCGGTTAATT TTACACATT AGTGCAATTGC 480
 55 GTATATCAAC TGGCCCTCAA TGAAGCATTT AAGTGCTTGG AATTTTACTA AACTGACTTT 540
 TTTGCAACTT TGGGAGATTT TTGAGGGGAG TGTGAAAT TGCCAAACAC TCACCTCTTA 600
 60 CTCAAACTT CAAATAAAAT ACACATTTTC AAGAGGGAGC ACCTTTTATA TTTGATAAGT 660

	TTTCATTATA AACCTTATAA TACCAGTCAC AAAGAGGTTG TCTGTCTATG GTTTAGCAAA	720
5	CATTTGCTTT TCTTTTGGGA AGTGTGATG CAATTGCAGA ACAGAAAGTG AGAAAACACT	780
	GCCAGCGGTG ATTGCTACTT GAGGTAGTTT TTTACAACATA CCATTTCCCC TCCATGAAAT	840
	TATGTGAAAT TTATTTTATC TTTGGGAAAA GTTGAGAAGA TAGTAAAAGA ATTAGGAATT	900
10	TAAAATTACA GGGAAAAATA TGTAAGTGAA AAGCAATAAA TATTTTGTTT ACTTTGCTAT	960
	CAAGATGTTT ACTATCAGAT ATTTATTATA TGGCAGCAAT TTATATTTT AATCATTGCC	1020
15	CATTAATAGA CGCAGTAAAA TATTTTGTGA TCAGACATTT GGGGTTTGTA TGTGCATTAA	1080
	AATTGTCTTT TGTACTGTAA GTTACTGTTA ATTTGAATAT TTTATTGAAC TGTCTCCCTG	1140
	TGCCTTTATA ATATAAAGTT GTTCTACAA CTTTAAATGA TCTTAATAAA GAATACTTTA	1200
20	AGAAAAAAAA AA	1212

25 (2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2061 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

35	GGTTTTCTC CGACTTCCGG ACATCTCCCT GGGAGTCGG CAGAGTGGAG TCAAAGGCAA	60
	CCAGTGCTCG CTGCGGTCTC TGGGGATCGG GACCGCGCG GCGGCCCGG AGCGGGATGT	120
40	TCCGGGGCTT GAGCAGTTGG TTGGGCTTGC AGCAGCCGGT GGCAGGCGGT GGGCAGCCCA	180
	ATGGAGATGC TCCACCCGAG CAGCCGTCCG AGACGGTGGC TGAGTCTGCG GAGGAGGAGC	240
	TGCAGCAAGC GGGAGACCAG GAGCTCCTCC ACCAGGCCAA AGACTTCGGC AACTATTTAT	300
45	TTAACTTTGC ATCTGCTGCC ACAAAAAAGA TAACTGAATC AGTTGCTGAA ACAGCACAAA	360
	CAATAAGAA ATCCGTAGAA GAAGGAAAAA TAGATGGCAT CATTGACAAG ACAATTATAG	420
50	GAGATTTTCA GAAGGAACAG AAAAAATTTG TTGAAGAGCA ACATACAAAG AAGTCAGAAG	480
	CAGCTGTGCC CCCATGGGTT GACACTAACG ATGAAGAAAC AATTCAACAA CAAATTTTGG	540
	CCTTATCAGC TGACAAGAGG AATTTCCCTC GTGACCCTCC GGCTGGCGTG CAATTTAATT	600
55	TCGACTTTGA TCAGATGTAC CCCGTGGCCC TGGTCATGCT CCAGGAGGAT GAGCTGCTAR	660
	CAAGATGAGA TTTGCCCTCG TTCTTAACT TGTGAAGGAA GAAGTGTCTT GGAGGAACTA	720
60	CTTTTACCGC GTCTCCCTGA TTAAGCAGTC AGCCCAGCTC ACGGCCCTGG CTGCCCCA	780

	GCAGGCCGCA GGGAAGGGAG GAGAAGAGCA ATGGCAGAGA GCAAGATTG CCGCTGGAGA	840
	GGCAGTACGG CCCAAAACGC CACCCGTTGT AATCAAATCT CAGCTTAAAA CTCAAGAGGA	900
5	TTAGGAAGAA ATTTCTACTA GCCCAGGTGT TTCTGAGTTT GTCAGTGATG CCTTCGATGC	960
	CTGTAACTTA AATCAGGAAG ATCTAAGGAA AGAAATGGAG CAACTAGTGC TTGACAAAAA	1020
10	GCAAGAGGAG ACAGCCGTAC TGGAAGAGGA TTCTGCAGAT TGGGAAAAAG AACTGCAGCA	1080
	GGAACCTCAA GAATATGAAG TGGTGACAGA ATCTGAAAAA CGAGATGAAA ACTGGGATAA	1140
	GGAAATAGAG AAAATGCTTC AAGAGGAAAA TTAGCTGTTC CTGAAATAGA AGAATAATCC	1200
15	TTAACAGTCT GCAAACGTAC ATTAATTTCT AGATGTTGAC AATTACTGAA TCAGAAGGCA	1260
	TGAAAGAGTA TAATTTTATG AAATTCAAAA TTATCTTTTT TTCAAGTTGA AACTTGCCCTC	1320
20	TTCTACTTTA AAAAAGTATA TAGAACAGTT ACTTCTAATA ATCAGAAAGA GATGTTTTAT	1380
	AGAACATTTT TTTAATATAA AGTTAGAGAT GTCTTCATAG GCAGTATGGC TATCTTTGCC	1440
	ACAGAAACAT AAGTAAATTT TTAGAGTTCT GTTTTCCATG AGGTCAAAAA TATAATTTAT	1500
25	TCCTCAGTCA TGGTTTTCTA AATATCTGTA CTCCACATTC CATTTTAATT GATATGAGGG	1560
	TGTTAAAGTA CCTACTTAAT GGGTTGATTA CTATCAAAAT GACCAAATTA TACCAAAGAA	1620
30	CTTAAGAGGA AGCACTTTCA GAACTATTCA CTTGCCAGGT ATTTTCTAAA ATTCCACCTG	1680
	AAAGCCAAAA GATAAAATAC ATNAGTTGGA TTTTAATGAT ATAAGCATCA CACAATTTTA	1740
	CATTAAGAAA TACTGTGCAG CCCATGCGTG GTGGCTCAGG CCTGTAATCC CAGCANTTTG	1800
35	GGAGGCCGAG GTGGGCAGAT CACCGGAGGT CAGGAGTTTC AGACCAGCCT TGCCAACATA	1860
	GTGAAACCTT GTCTTTACTA AAAATACAAA AATTAGCCGG GCATGGTGGC AGGCACCTGT	1920
40	AATCCCAGCT ACTAGGGAGG CTTTGAACC CAGGAGGCAG AGGTTCGAGC GAGCTGAGAT	1980
	CGCGCCACTG CACTCCAGCC TGGGTGATAG AGTGAGATTC AGTCTCAAAA AAAAAAAAAA	2040
	AAAAAAAAAA AATGACCTCG A	2061

45

(2) INFORMATION FOR SEQ ID NO: 15:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

	CCCTTCATCT GCGTTGCCAG GAACCTGTG AGCAGAACT TCTCAAGCCC CATCCTTGCC	60
60	AGGAAGCTCT GTGAAGGTGC TGCTGATGAC CCAGATTCCT CCATGGTCCT CCTGTGTCTC	120

CTGTTGGTGC CCCTCCTGCT CAGTCTCTTT GTACTGGGGC TATTTCTTTG GTTTCTGAAG 180
 5 AGAGAGAGAC AAGAAGAGTA CATTGAAGAG AAGAAGAGAG TGGACATTTG TCGGGAAACT 240
 CCTAACATAT GCCCCCATTC TGGAGAGAAC ACAGAGTACG ACACAATCCC TCACACTAAT 300
 AGAACAATCC TAAAGGAAGA TCCAGCAAAT ACGGTTTACT CCACTGTGGA AATACCGAAA 360
 10 AAGATGGAAA ATCCCCACTC ACTGCTCAGC ATGCCAGACA CACCAAGGCT ATTTGCCTAT 420
 GAGAATGTTA TCTAGACAGC AGTGCCTCC CCTAAGTCTC TGCTCAAAAA AAAACAATT 480
 CTCGGCCCAA AGAAAACAAT CAGAAGAATT CACTGATTTG ACTAGAAACA TCAAGGAAGA 540
 15 ATGAAGAACG TTGACTTTTT TCCAGGATAA ATTATCTCTG ATGCTTCTTT AGATTTAAGA 600
 GTTCATAATT CCATCCACTG CTGAGAAATC TCCTCAAACC CAGAAGGTTT AATCACTTCA 660
 20 TCCCAAAAAT GGGATTGTGA ATGTCAGCAA ACCATAAAAA AAGTGCTTAG AAGTATTCCT 720
 ATAAAAATGT AAATGCAAGG TCACACATAT TAATGACAGC CTGTTGTATT AATGATGGCT 780
 CCAGGTCAGT GTCTGGAGTT TCATTCCATC CCAGGGCTTG GATGTCAGGA TTATACCAAG 840
 25 AGTCTTGCTA CCAGGAGGGC AAGAAGACCA AACAGACAG ACAAGTCCAG CAGAAGCAGA 900
 TGCACCTGAC AAAAATGGAT GTATTAATTG GCTCTATAAA CTATGTGCCC AGCAYTATGC 960
 30 TGAGCTTACA CTAATTGGTC AGACATGCTG TCTGCCCTCA TGAAATTGGC TCCAAATGAW 1020
 TGAACACTT TCATGAGCAG TTGTAGCAGG CCTGACCACA GATTCCCAGA GGGCCAGGTG 1080
 TGGATCCACA GGACTTGAAG GTCAAAGTTC ACAAAGATGA AGAATCAGGG TAGCTGACCA 1140
 35 TGTMTGGCAG ATACTATAAT GGAGACACAG AAGTGTGCAT GGCCCAAGGA CAAGGACCTC 1200
 CAGCCAGGCT TCATTTATGC ACTTGTCTGC AAAAGAAAAG TCTAGGTTTT AAGGCTGTGC 1260
 40 CAGAACCCAT CCCAATAAAG AGACCGAGTC TGAAGTCACA TTGTAAATCT AGTGTAGGAG 1320
 ACTTGAGATC AGGCAGTGAG ACTGGTGGGG CACGGGGGGC ANTGGGTANT GTAAACCTTT 1380
 45 TAAAGATGGT TAATTCNTCA TTAGTGTTTT TT 1412

(2) INFORMATION FOR SEQ ID NO: 16:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

60

TTCCTCTCCT CTCTCTACCC CTCCTGTCTC TCCTCCCCTC CTCTCTCTTC CTCTCCTCTC 60

	TCTCTTCCTC TCCTCTCTCT TCCCTTCCTG TCTCTCTTCC CCTCCTCTCT CTCTTCCTGT	120
	CCTCTATCTC TTCCCCTCCT CTATCTCTTC CTCTCCTCTC TCTCTTCCTC TCCTCTCTCT	180
5	CTCTTSCFTT CTCTCTCTCT TCCTGTCTCG GCTGTGTGG GTTGACAGTT GGGTGCTGCT	240
	GTTGTGGTCC TTCCCAGAAA CTGCCAGTAG AGGGCAGCCT GGGCATCCTA ATGCTTACTC	300
10	TGGTTGTTAC ACAAAGAAAA TATTGGGGTC ACTGGCGAGC CCACCCACAC TCACCAGAAT	360
	CTCCACTGTA GTCCCCCTAA CAAACAGCCC TTCACTTCCT CTCCCACTTC AGCAATTGTG	420
	ATTTTGATGC CATTTGGCTC AGATCAGAGT GTTTTAAATC ATCACGCCCT GGCTTATCCC	480
15	TGGTCGAGCC AGGACACGGG GTGCTTCAGT GGGTCTGTCA CCTCTCTCC TTGAAGCATG	540
	TGCTTTTAT TTATTTACTT TTACTCTCAC CCTGCTCCTG TACCAGCAGG GGCCACTTCA	600
20	AAGCCAAGGT ACAGGGTGAT AACTTGTGGT CCAGCATCAG TTTTCTCCAC TTCTTTCTCC	660
	CACTCACCCC CAGCAAGGTG CCTGGGGAGA CTTGAGCAGA TGTTCATTG TGGCCTGGCC	720
	AGTGCTGAA AGCAGGCCTC CAATGCACTG TGACCTCTGG CTTCCTCAGC AGCTTTCCCA	780
25	GAGAGGCAGA GGGGCCTTCC ACAGCCCGGG TTCTCCTGCT GCCTCCTGCC TGCTGCAGCT	840
	GCAGGCATTG TGAGGGGCAA CGTGGAGGAA GGGCCAGGGA TGCATGGGAT TTTAATTGTT	900
30	TCATCACACC TTCCCCGTGG CAAAGAAACA GTCAGTCCTC TTCAGGTGTC TTCTGGATTT	960
	CTGGTGATGG ACAGAGAAAT CTTTTTACAG TTTCAAATTA TGTCAACAA ATAAAAATTG	1020
	CATTTTAT TTTGAAAAA AAAAAAAAAA AA	1052
35		

(2) INFORMATION FOR SEQ ID NO: 17:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

	AATTCGGCAG AGGCACTTAT CATGTACATA TAGCCTGTTT TTTAGCATTG TTAGACAAAG	60
50	TAGGCATATT CCTTCCATC CAAGAACTCA TAACCTAGTA ATTGTAGTTG GCTGATAGCT	120
	CATTGCCCAT ACACAAGGAT CTAACACAAC CTCTTGAATA AACATCCCCC TTATTACAGAA	180
55	ATGCCTTTTC CTATTCCAT ATTGCAACTT TGCTTACAAA TTTCCAATCT GTCTTTCTGT	240
	TTACAGAAGA TATACAAAAT TCCTTTTGTA TGATCTCTTT ATATCTCTTG ATTTTCTTTT	300
	GTGTTTGCTA CCAAAGGGCC TGCACATAGT GAGAAGATTG TGCATGATCT GTGAGCTCTA	360
60	CCACACCTGG AATTAGGGAT CACCAATATG AGAAAAAAAA TTGGAGGTAC AAATAACATT	420

ATCATATGTW ATTGGCATAT AAATTACAGA TGTWCTATG ACTAAAACC CTGTGGATAT 480
 WAACMAATG CAGATAAWTW TAATAAAATW TWTAAAAATW TWATCMAATA ATGATAGTGC 540
 5 TATTCAAATA CTTCAAATTT GCACAGTGAT TTATTTCTTA AAATATGTTA ACACATGTGA 600
 GCCAATACAC TGAGGTCACCT GGATAAATAA ACAGATTCTT GCAAAAAAAA AAAAAAAAAA 660
 10 ACTCGAGGGG GGCCCGTACC CTT 683

15 (2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1054 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

25 AAACATTTT AGGTGACACT ATAGAAGGTA CGCCTGCAGG TACCGGTCCG GAATTCCTCGG 60
 GTCGACCCAC GMGNCCGGCG ACAAGATGGC AGCAGCGTGT CGGAGCGTGA AGGGCTTGGT 120
 GGCGGTAATA ACCCGAGGAG CCTCGGGCCT GGGCCTGGCC ACGCGGACG ACTTGTGGGG 180
 30 CAGGGAGCCT CTGCTGTGCT TCTGGACCTG CCCAACTCGG GTGGGGAGGC CCAAGCCAAG 240
 AAGTTAGGAA ACAACTGCGT TTTCGCCCCA GCCGACGTGA CCTCTGAGAA GGATGTGCAA 300
 35 ACAGCTCTGG CTCTAGCAAA AGGAAAGTTT GGCCGTGTGG ATGTAGCTGT CAACTGTGCA 360
 GGCATCGCGG TGGCTAGCAA GACGTACAAC TTAAAGAAGG GCCAGACCCA TACCTTGAA 420
 GACTTCAGC GAGTTCTTGA TGTGAATCTC ATGGGCACCT TCAATGTGAT CCGCCTGGTG 480
 40 GCTGGTGAGA TGGGCCAGAA TGAACCAGAC CAGGGAGGCC AACGTGGGGT CATCATCAAC 540
 ACTGCCAGTG TGGCTGCCTT CGAGGGTCAG GTTGGACAAG CTGCATACTC TGCTTCCAAG 600
 45 GGGGAATAG TGGGCATGAC ACTGCCCATT GCTCGGGATC TGGCTCCCAT AGGTATCCGG 660
 GTGATGACCA TTGCCCCAGG TCTGTTTGGC ACCCCACTGC TGACCAGCCT CCCAGAGAAA 720
 GTGTGCAACT TCTTGCCAG CCAAGTGCCC TTCCCTAGCC GACTGGGTGA CCCTGCTGAG 780
 50 TATGCTCACC TCGTACAGG CATCATCGAG AACCCATTCC TCAATGGAGA GGTATCCGG 840
 CTGGATGGGG CCATTCTGAT GCAGCCTTGA AGGGAGAAGG CAGAGAAAAC ACACGCTCCT 900
 55 CTGCCCTTCC TTTCCCTGGG GTACTACTCT CCAGCTTGGG AGGAAGCCCA GTAGCCATTT 960
 TGTAAGTACC TACCAGTCGC CCTCTGTGCC TAATAAAGTC TCTTTTCTC ACANAAAAA 1020
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 1054
 60

(2) INFORMATION FOR SEQ ID NO: 19:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

15	GGAACAAGCT GGGATATGTG AGCGTTAAGC TACTCACATC CTTCAAAAAG GTGAAACATC	60
	TTACACGGGA CTGGAGAACC ACAGCACATG CTTTGAAGTA TTCAGTGGTC CTTGAGTTGA	120
	ATGAGGNCCA CCGGAAGGTG AGGAGGACCA CCCCCGTCCC ACTGTTCCCC AACGAGAACC	180
20	TCCCCAGCAA GATGCTCCTG GTCTATGATC TCTACTTGTG TCCTAAGCTG TGGGCTCTGG	240
	CCACCCCCCA GAAGAATGGG AAGGGTGCAA GARAAGGTGA TGGAACACCT GCTCAAGCTT	300
	TTTGGGACTT TTGGAGTCAT CTCATCAGTG CGGATCCTCA AACCTGGGAG AGAGCTGCCC	360
25	CCTGACATCC GGAGGNTCCA GCAGCCGCTA CAGCTCCTCT GACCCCGAGA GCAACCCAC	420
	ATCCCTATG GCGGGCCGAC GGCACGNGKC CACCAACAAG CTCAGCCCGT CTGGCCACCA	480
30	GAATCTCTTT CTGAGTCCAA ATGCCTCCCC GTGCACAAGT CCTTGGAGCA GCCCCTTGGC	540
	CCAACGCAAA GCGGTTTCCA GAAAGTCCCC ACTGGCGGAG GAAGGTAGAC TGAAGTGCAG	600
	CACCAGCCCT GAGATCTTCC GCAAGTGTAT GGATTATTCC TCTGACAGCA GCGTCACTCC	660
35	CTCTGGCAGC CCCTGGGTCC GGAGGCGTCG CCAAGCCGAG ATGGGGACCC AGGAGAAAAG	720
	CCCCGGTACG AGTCCCCTGC TCTCCCGGAA GATGCAGACT GCAGATGGGS TACCCGTAGG	780
40	TNGCTTGAGG TTGCCCAGGG GTCCTGACAA CACCAGAGGA TTTCATGGCC ATGAGAGGAG	840
	CAGGGCCTGT GTATAAATAC CTTCTATTTT TAATACAAGC TCCACTGAAA ACCACCTTCG	900
	TTTTCAAGGT TCTGACAAAC ACCTGGCATG ACAGAATGGA ATTCGTTCCC CTTTGAGAGA	960
45	TTTTTTATTC ATGTAGACCT CTTAATTTAT CTATCTGTAA TATACATAAA TCGGTACGCC	1020
	ATGGTTTGAA GACCACCTTC TAGTTCAGGA CTCCTGTTCT TCCCAGCATG GCCACTATTT	1080
50	TGATGATGGC TGATGTGTGT GAGTGTGATG GCCCTGAAGG GCTGTAGGAC GGAGGTTCCC	1140
	TGGGGGAAGT CTGTTCTTTG GTATGGAATT TTTCTCTCTT CTTTGGTATG GAATTTTTC	1200
	CTTCAGTGAC TGAGCTGTCC TCGATAGGCC ATGCAAGGGC TTCCTGAGAG TTCAGGAAAG	1260
55	TTCTCTTGTG CAACAGCAAG TAGCTAAGCC TATAGCATGG TGTCTTGTAG GACCAAATCG	1320
	ATGTTACCTG TCAAGTAAAT AAATAATAAA ACACCCAAC TGGAGTGCTG AAAAAAANA	1380
60	ANNAAAAAAC TCG	1393

5 (2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

15 AGGAAAAGTT TTCCNAATTG GAAAGCGGGC AGTGAGCGCA ACGCAATTAA TGTGAGTTAG 60
NTCANTCATT AGGCACCCCA GGCTTTACAC TTTATGCTTC CGGNTCGTAT GTTGTGTGGA 120
ATTGTGAGCG GATAACAATT TCACACAGGA AACAGCTATG ACCATGATTA CGCCAAGCTN 180
20 TAATACGACT CACTATAGGG AAAGCTGGTA CGCCTGCAGG TACCGGTCCG GAATTCCCGG 240
GTCGACCCAC GCGTCCGCCC ACGCGTCCGT GAAAATCCGA AGTGCCGCGG AAAGTGAGG 300
25 TGAGGGCCGC CCGCCCTAGA GGTGCCCGTC CGAGAGGCAG AGCTGACAAG GAAGGTTTCG 360
AGCGTTTTGC TGGCAAAGGG ATTCTTTACA ACCTCCAGGC ATGCGTCTTT CTGCCCTGCT 420
GGCCTTGGA TCCAAGGTCA CTCTGCCCCC CCATTACCGC TATGGGATGA GCCCCCAGG 480
30 CTCTGTTGCA GACAAGAGGA AGAACCCCC ATGGATCAGG CGGCGCCCAG TGGTTGTGGA 540
ACCCATCTCT GATGAAGACT GGTATCTGTT CTGTGGGGAC ACGGTGGAGA TCCTAGAAGG 600
35 CAAGGATGCC GGAAGCAGG GCAAAGTGGT TCAAGTTATC CGGCAGCGAA ACTGGGTGGT 660
CGTGGGAGGG CTGAACACAC ATTACCGCTA CATTGGCAAG ACCATGGATT ACCGGGGAAC 720
CATGATCCCT AGTGAAGCCC CCTTGCTCCA CCGCCAGGTC AAATTGTGG ATCCTATGGA 780
40 CAGGAAACCC ACTGAGATCG AGTGGAGATT TACTGAAGCA GGAGAGCGGG TACGAGTCTC 840
CACACGATCA GGGAGAATTA TCCCTAAACC CGAATTTCCC AGAGCTGATG GCATCGTCCC 900
45 TGAAACGTGG ATTGATGGCC CCAAAGACAC ATCAGTGGAA GATGCTTTAG AAAGAACCTA 960
TGTGCCCTGT CTAAAGACAC TGCAGGAGGA GGTGATGGAG GCCATGGGGA TCAAGGAGAC 1020
CCGGAATAC AAGAAGGTCT ATTGGTATTG AGCCTGGGGC AGAGCAGCTC CTCCCCAACT 1080
50 TCTGTCCCAG CCTTGAAGGC TGAGGCACTT CTTTTTCAGA TGCCAATAAA GAGCACTTTA 1140
TGAGTCCTCC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1200
55 AAAAGGGGCG GCCGC 1215

60 (2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2042 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

10	CTGCATCCAG GCGCAGAATA ACCTGGGTAT CTTGTGGTCT GAAAGAGAGA AATTGAAACT	60
	GCACAGGCTT ACCTAGAGTC ATCAGAAGCA CTATATAATC AGTATATGAA AGAGGTTGGG	120
	AGTCCTCCTC TTGATCCTAC TGAGCGTTTT CTTCTGAAGA AGAGAACTT ACTGAACAAG	180
15	AGAGATCAAA AAGATTGAA AAGGTTTATA CTCATAACCT ATATTACCTA GCTCAAGTCT	240
	ACCAGCATCT GGAAATGTTT GAGAAGGCTG CTCACTATTG CCATAGTACA CTAAAACGCC	300
20	AGCTTGAGCA CAATGCCTAC CATCCTATAG AGTGGGCTAT CAATGCTGCT ACCTTGTCAC	360
	AGTTTTACAT CAATAAGCTA TGCTTTATGG AGGCCAGGCA CTGTTTATCA GCTGCTAATG	420
	TCATTTTTGG TCAAAGTGA AAGATCTCAG CCACAGAAGA CACTCCTGAA GCTGAAGGAG	480
25	AAGTGCCAGA GCTTTATCAT CAAAGAAAGG GGGAAATAGC AAGGTGCTGG ATCAAATACT	540
	GTTTGACTCT CATGCAGAAT GCCCAACTCT CCATGCAGGA CAACATAGGA GAGCTTGATC	600
30	TTGATAAACA GTCTGAACTT AGAGCTTTAA GGAAAAAGA ACTAGATGAG GAGGAAAGCA	660
	TTCGGAAAAA AGCTGTGCAG TTTGGAACCG GTGAACTGTG TGATGCCATC TCTGCAGTAG	720
	AAGAGAAAGT GAGCTACTTG AGACCTTTAG ATTTTGAAGA AGCCAGAGAA CTTTTCTTAT	780
35	TGGGTGAGCA CTATGCTTTT GAGGCAAAAG AGTTCTTTCA GATTGATGGT TATGTCAGTG	840
	ACCATATTGA AGTTGTCCAA GACCACAGTG CTCTGTTTAA GGTGCTTGCA TTCTTTGAAA	900
40	CTGACATGGA GAGACGGTGC AAGATGCATA AACGCRGAAT AGCCATGCTA GAGCCCCTAA	960
	CTGTAGACCT GAATCCACAG TATTATCTGT TGGTCAACAG ACAGATCCAG TTTGAAATTG	1020
	CACATGCTTA CTATGATATG ATGGATTGGA AGGTGTCAT TGCTGACAGG CTAAGGGATC	1080
45	CTGATTCACA CATTGTAATA AAAATAAATA ATCTTAATAA GTCAGCACTG AAGTACTACC	1140
	AGCTCTTCTT AGACTCCCTG AGAGACCCAA ATAAAGTATT CCCTGAGCAT ATAGGGGAAG	1200
50	ATGTTCTTCG CCCTGCCATG TTAGCTAAGT TTCGAGTTGC CCGTCTCTAT GGCAAAATCA	1260
	TTACTGCAGA TCCCAAGAAA GAGCTGGAAA ATTTGGCAAC ATCATTGGA ACATTACAAA	1320
	TTTATTGTTG ATTACTGTGA AAAGCATCCT GAGGCCGCC AGGAAATAGA AGTTGAGCTA	1380
55	GAACCTTAGTA AAGAGATGGT TAGTCTTCTC CCAACAAAAA TGGAGAGATT CAGAACCAAG	1440
	ATGGCCCTGA CTTAATCCTT GTTTTAAAG AAAGGAAATG TGCAATATTG AAGTGATCTT	1500
60	TTTCCCTAGT CAGACAGGCC CAATTCCATT GTGATGTTTA CCTTTATAGC CAGGTGAGTG	1560

CAGTTTGAAC TTGAGATACA GTCAACTGAG TGTTTGCTAG GATCCTAAGG AACATAAAGT 1620
 TAATTAAAAA CTTACACCTA APTATGTAAA TTGCCTTGTT AAAGACATGT GATTGTGTATT 1680
 5 TTAGATGCTT GTTTCCTATT AAAATACAGA CATTTCTACC CTCAGTTTCT AAATGTAGAC 1740
 TATTGTGG CTAGTACTTG ATAGATTCCT TGTAAGAAAA AATGCTGGGT AATGTACCTG 1800
 10 GTAACAAGCC TGTAAATATA TTAAGATTGA AAAAGTAACT TCTATAGTTA CTCCTTCTAA 1860
 AATATTTGAC TTCCTACATT CCCCCACCC AAAATCTTTC CCTTTTGAAA ATACTAAAAA 1920
 CTAAGTTATG TTATTATAAA GTGTAAAATG GTTTGTCTTA ATTATAGGAG AAAAAGGCCT 1980
 15 TGTTAGAAAT AAAATAAACT GACTTATTTT ACTAATGAAA AAAAAAAAAA AAAAAAAAAA 2040
 TT 2042
 20

(2) INFORMATION FOR SEQ ID NO: 22:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1872 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GGGTCGACCC ACGCGTCCGA TTGGCCTAGA GTCCTGTGA CCGAGAGCGC CACGGAAGCC 60
 35 TGGGGATGAT GTCGGGCAGC TTTATTCTTT GCTTGGCTTT GGTAAC TAGG TGGTCCCCTC 120
 AAGCATCCTC AGTTCCTCTT GCTGTTTATG AATCTAAGAC AAGGAAGTCC TATAGAAGCC 180
 40 AAAGGGACAG GGACGGAAG GACAGGTCCC AAGGGATGGG GCTGTCCTTA CTTGTGGAAA 240
 CCAGGAAATT GTCCTCTCA GCCAACCAAG GTTGACCACA CACCACCCTT CCGGAGCAGC 300
 TCAGTCAGCC CTCGGGGACG RGAAACCACA AGCGCAGAGA CGCTGAGGCC CAGGCAGGTG 360
 45 AAGAGGAAGT GGCTTTGGGT TTTTAAAGTA GGTGAGCGTG ACCTCTCTGA CTGCTTCTTC 420
 CCGGGGGGGG ACTGCAAACC GCTCAGGGTT GCGGCAGAGC CATGGACTTC CGGTCCCTGC 480
 AACGGGTGAC CTAAGCGTGG TGCACCCATC AGTCACGCAG GAGGACTGAC TTGACAGACG 540
 50 AAAGACAAGC CCGGATGACA CAGGGTGAGA AGAGTCAGGG CCGCACCTCT GTCCCTGCAA 600
 ACCAACAGGT GCATGGTGAG TGTGGCAGTC CCCACAGCTC CACAATGGGC TCCCCGCCA 660
 55 ACGGGGACGA CAGGGATCTT CAGGAACTTC TGACCTCACC AAGTCAAGTG GACCACTCTC 720
 CACTCCACGA GGATGTGAAA CGGTTCTTTA AAATGGGATT TTAGAGCCTC GGAATGCAT 780
 60 GTGCGTCGCA TCTTTCATAT TATGGGTCAG GATAGATTCA TTTCTTGCAA CATAGTGGA 840

	AAGATATAAG CTGCAGTAAT TTGCTCTTTG AATGACCGTC ACCCCCAGTA TAGGATATGC	900
	TTGTATCCCC CCGTCACTCC TCCGCCTGTT TTTTAAACTT TTCCACCACC TCGTCCAAA	960
5	AAGAATGTTA TAGCGAGTGC TCTTAAATGT TGAACCTGGG TGTTCCTTCC GGGCCAGTCT	1020
	GCGTGGCTCC ATGAAAAGCT CACTGCTGCC CCAGCCGGGC TTCTTAGAGG AGGTCAGTTG	1080
10	TCCTATGTAT CATCATTTAC TCTGGGAATC CTA CTGTGAA ATCATGTCTG TATTTTCTG	1140
	GAGCAGTTCA CATAGAGTAG AATGTGGAAT TTCCCGTGAA CGTCTCCTTC CTCCCCGTA	1200
	TCTGCCGCTT GTCACCTCGC CACCGTGCTA GAATACTGTT GTGTTGTAAG ATGACTAATT	1260
15	TTAAAGAAG CTGCCCTGAA AAGTTCTTAG AAACGCAATG AAAGGGAGGA ACTTGTCTT	1320
	TACCCAGTTT TTCCTTTGTA GGATGGGAAA GTATAAAAAG GCACAGAAGG TTGTCATGGG	1380
20	CTGTTCTCTG GGGGTTTTTA TCCTGCTCAC CGTGGAGATA AGCCTGCGGC TTGTCTAACC	1440
	AGCGCAGCGM AAAGGTCTCA ATGCCCTTTG GTAACATCCG TCATTGCAGA AGAAAGTTTA	1500
	CACGACGTCA AAAAGTGACG TTCATGCTAA GTGTTTTCAG AAATATATG GTTTCATGTT	1560
25	TCTTATTKGC TCTGCCTCCT GTGCTTATAT CATCCAAAAA CTTTTTAAAA AGGTCCAGAA	1620
	TTCTATTTTA ACCTGATGTT GAGCACCTTT AAAACGTTTCG TATGTGTGTT GCACTAATTC	1680
30	TAAACTTTGG AGGCATTTTG CTGTGTGAGG CCGATCGCCA CTGTAAAGGT CCTAGAGTTG	1740
	CCTGTTTGTC TCTGGAGATG GAATTAAACC AAATAAAGAG CTTCCACTGG AGGCTTGAT	1800
	TGACCTTGTA ACTATATGTT AATCTCGTGT TAAATAAAAA TATAACTTGT GAAAAAAAAA	1860
35	AAAAAAAAAC NT	1872

40 (2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 289 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

50	CATTTACCCA CCTATCAACA TGTTCGTTT CTCTTTTGTG GGTGAGAATG AGTGGCTTCT	60
	TGCTCCTAGC TAGAGCCAGT CCTCCATAT GTGCTTTAGA TTCTTCCTGT TTTGTTCAAG	120
	AATATGCTC AAGCTATTCT TCCTCCTGTT TCCTGCATCA GCATTTCCCC TCTCTACTAG	180
55	ATCATCTCTG TCAGTAAATG AACATGTTGT TGTTCCTCT AGAAGTACTG TTTCTATATC	240
	TAGATAGTAC TCTAGCTAGA GTTAAAAAAA AAAAAAAAAA CCTNGGGGG	289

60

(2) INFORMATION FOR SEQ ID NO: 24:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3533 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

	TTTTATTTAC TTCAATTTAA CTGTACTTTA CTCAAATAGA AAANGAATAA TTTTCACATT	60
15	ATGAAGCTAC ACAATTCCAA AATACACATG CTGAGGCTCT TTTTAAGTCC GAATTGTCTA	120
	GTAATTACAA AAAAGTGAAG AGTTTACAGA TATACAAGGA AATAAAGGCG AATTATTGCA	180
20	AAGAAAACAA GTTTAATTTT ACTTTGAATG ACAACGATTT TTCTGGAAAG CAGATACTTC	240
	ACTCCTTTAA GTTTCCACCC AAGCCACAAT AATTTCAAAC GGTCTTGCGG ATGACCCAGC	300
	TGGTCACTCT TGTTTATGTG GGGACTGGAG GTAATGAGAG CCAAAAAAAG TGCTATAAAC	360
25	CTAATTTGGC TAGAGCAAGT TCACACGACA CGACCGTGCT TTAAAACTT GCTCTCCATT	420
	ATGTACTTCC TTCCATCAGG TTGGGGAAAA AAAAATGGTG GGGATGGTGA GTAAACACAC	480
	CAGTGGTTTC ATCAGAGGGG AACTCACTAC TCAGGAGGTG ACGGTGACGT GGTGCCGGTC	540
30	CCTGAAGTAC GCGCACAAGC TCCGGAGGTT GCGGGAGCTT CCGCTGCCGC CTGAGGGGAA	600
	GCCGGAGCGA CGGGGGTCAC GCGGGCGGTC AGAGGGTAAA GGTCTTGCTC CCAGCAGCCT	660
35	CCGCGGTGGA TACGTCGCCA TCTTGGATCC GCGGGACAAG AAAATTCATG CGAGGGAGAC	720
	GTGGTGGCG GTCTTCTCTG TGACACGACC CTTGAGTGAC AGTTCTATTT GATTGCCTCC	780
	GGTACTGTGA GGAAAGGACA CGACTCTATG GTGAGGACTG ATGGACATAC ATTATCTGAG	840
40	AAAAGAACT ACCAGGTGAC AAACAGCATG TTTGGTGCTT CAAGAAAGAA GTTTGTAGAG	900
	GGGGTCGACA GTGACTACCA TGACGAAAAC ATGTACTACA GCCAGTCTTC TATGTTTCCA	960
45	CATCGGTCAG AAAAAGATAT GCTGGCATCA CCATCTACAT CAGGTCAGCT GTCTCAGTTT	1020
	GGGGCAAGTT TATACGGGCA ACAAAGTGCA CTAGGCCTTC CAATGAGGGG GATGAGCAAC	1080
50	AATACCCCTC AGTTAAATCG CAGCTTATCA CAAGGCACTC AGTTACCGAG CCACGTCACG	1140
	CCAACAACAG GGGTACCAAC AATGTCACCT CACACGCCTC CATCTCCAAG CAGGGGTATT	1200
	TGCTCTATGA ATCTTARGAA TATGATGAAC CACTCCAGG TTGGTCAGGG CATTTGAATT	1260
55	CCTAGCAGGA CAAATAGCAT GAGCAGTTCA GGGTTAGGTA GCGGCAACAG AAGCTCGCCA	1320
	AGCATAATAT GTATGCCAAA GCAGCAGCCT TCTCGACAGC CTTTACTGT GAACAGTATG	1380
60	TCTGGATTG GAATGAACAG GAATCAGGCA TTTGGAATGA ATAACCTCTT ATCAAGTAAC	1440

	ATTTTAAATG GAACAGACGG AAGTGAAAAT GTGACAGGAT TGGACCTTTC AGATTTCCTCA	1500
	GCATTAGCAG ACCGAAACAG GAGGGAAGGA AGTGGTAACC CAACTCCATT AATAAACCCC	1560
5	TTGGCTGGAA GAGCTCCTTA TGTGGAATG GTAACAAAAC CAGCAAATGA ACAATCCAG	1620
	GACTTCTCAA TACACAATGA AGATTTTCCA GCATTACCAG GCTCCAGCTA TAAAGATCCA	1680
10	ACATCAAGTA ATGATGACAG TAAATCTAAT TTGAATACAT CTGGCAAGAC AACTTCAAGT	1740
	ACAGATGGAC CCAAATTTCC TGGAGATAAA AGTTCAACAA CACAAAATAA TAACCAGCAG	1800
	AAAAAAGGGA TCCAGGTGTT ACCTGATGGT CGGGTTACTA ACATTCTCTCA AGGGATGGTG	1860
15	ACGGACCAAT TTGGAATGAT TGGCCTGTTA ACATTTATCA GGCAGCAGA GACAGACCCA	1920
	GGAATGGTAC ATCTTGCAAT AGGAAGTGAC TTAACAACAT TAGGCCTCAA TCTGAACTCT	1980
20	CCTGAAAATC TCTACCCCAA ATTTGCGTCA CCCTGGGCAT CTTCACCTTG TCGACCTCAA	2040
	GACATAGACT TCCATGTTCC ATCTGAGTAC TTAACGAACA TTCACATTAG GGATAAGCTG	2100
	GCTGCAATAA AACTTGGCCG ATATGGTGAA GACCTTCTCT TCTATCTCTA TTACATGAAT	2160
25	GGAGGAGACG TATTACAAC TTTAGCTGCA GTGGAGCTTT TTAACCGTGA TTGGAGATAC	2220
	CACAAAGAAG AACGAGTATG GATTACCAGG GCACCAGGCA TGGAGCCAAC AATGAAAACC	2280
30	AATACCTATG AGAGGGGAAC ATATTACTTC TTTGACTGTC TTAAGTGGAG GAAAGTAGCT	2340
	AAGGAGTTCC ATCTGGAATA TGACAAATTA GAAGAACGGC CTCACCTGCC ATCCACCTTC	2400
	AACTACAACC CTGCTCAGCA AGCCTTCTAA AAAAAAAAAA AAAAAAAAAA AAAAAGACTT	2460
35	CCCTTTTCTT GGGGTATGGC TGTCTCAGCA CAATACTCAA CATAACTGCA GAACTGATGT	2520
	GGCTCAGGCA CCCTGGTTT AATTCCCTGA GGATCTGGCA ATTGGCTTAC GCAAAAGGTC	2580
40	ACCATTTGAG GTCCTGCCTT ACTAATTATG TGCTGCCCAA CAACTAAATT TGTAATTTGT	2640
	TTTTCTCTAG TTTGAGCAGG GTCCTGAATTT TTTTATTTAT TTCCTTTTTT GCCAGCAGAC	2700
	AGACTTGAGT CTGTAAAGAC AAGCAAATAC ACTGACAGAA GTTTACCATA GTTTCTAAAA	2760
45	TGTAAAAAAG AAAACCCCCA AAAGACTCAA GAAAATTAGA CCACAAATTT TGCATTGTTC	2820
	ATTGTAGCAC TATTGGTAAT AAAATAACAA ATGTTTGTGC ATTTTATATGT GAAGATCCTT	2880
50	CTCGTATTTT ATTTGGAAAG ATGAGCAAGA GGTCTGCTTC CTTTATTTTA CTTCCTCTTC	2940
	TGTTTTTGAA AGGCAGTTTC GCCAAGCTTA ATGCAAGAAT ATCTGACTGT TTAGAAGAAA	3000
	GATATTGCCA CAATCTCTGG ATGGTTTCC AGGGTTGTGT TATTACTGAG CTTCATCTTT	3060
55	CCAGAATGAG CAAAACACTG TCCAGTCTTT GTTACGATTT TGTAATAAAT GTGTACATTT	3120
	TTTTTAAATT TTTGGACATC ACATGAATAA AGGTATGTAT GTACGAATGT GTATATATTA	3180
60	TATATATGAC ATCTATTTTG GAAAATGTTT GCCCTGCTGT ACCTCATTTT TAGGAGGTGT	3240

GCATGGATGC AATATATGAA AATGGGACAT TCTGGAAC TGCTGTCAGGG GACTTTGTCTG 3300
 CCCTGTGCAC TAAAAGGGCC AGATTTTCAG CAGCCAAGGA CATCCATACC CAAGTGAATG 3360
 5 TGATGGGACT TAAAAGAAGT GAACTGAGAC AATTCAC TCT GGCTGTTTGA ACAGCAGCGT 3420
 TTCATAGGAA GAGAAAAAAA GATCAATCTT GTATTTTCTG ACCACATAAA GGCTTCTTCT 3480
 10 CTTTGTAATA AAGTAGAAAA GCTCTCCTCA AAAAAAAAAA AAAAAAACTC GAG 3533

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1148 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCCACGCGT CCGCAAATTA TACTTCCTCA TTCATATTAT GTTGATACAA AAGACCTTGG 60
 25 CAGCCATTTC TCCCAGCAGT TTTAAAGGAT GAACATTGGA TTTCATGCCA TCCCATAGAA 120
 AACCTGTTTT AAAATTTT TAGTCTTTAC TTGGTCATAC ATGAAAAGTA CACTGCTTAG 180
 30 AAATTATAGA CTATTATGAT CTGTCCACAG TGCCCATTTGT CACTTCTTTG TCTCATTTCT 240
 TCCCTTTGTT CCTTAGTCAT CCAAATAAGC CTGAAAACCA TAAGAGATAT TACTTTATTG 300
 AATATGGTTG GCATTAAATT TAGCATTTCA TTATCTAACA AAATTAATAT AAATTCCAGG 360
 35 ACATGGTAAA ATGTGTTTTA ATAACCCCCA GACCCAAATG AAAATTTCAA AGTCAATACC 420
 AGCAGATTCA TGAAAGTAAA TTTAGTCCTA TAATTTTCAG CTTAATTATA AACAAAGGAA 480
 40 CAAATAAGTG GAAGGGCAGC TATTACCATT CGCTTAGTCA AAACATTCGG TTAGTCCCCT 540
 TTAATACACT CCTATCATCA GCACTTCCAC CATGTATTAC AAGTCTTGAC CCATCCCTGT 600
 CGTAACTCCA GTAAAAGTTA CTGTTACTAG AAAATTTT TCAATTAACT GACAAATAGT 660
 45 TTCTTTTAA AGTAGTTTCT TCCATCTTTA TTCTGACTAG CTTCCAAAAT GTGTTCCTT 720
 TTTGAATCGA GGTTTTTTTG TTTTGTTTTG TTTTCTGAAA AAATCATACT ACTTTGTGCT 780
 50 TCTATTGCTT TTTTGTGTTT TGTTAAGCAT GTCCCTTGCC CCAAATGGAA GAGGAAATGT 840
 TTAATTAAATG CTTTTTAGTT TAAATAAATT GAATCATTTA TAATAATCAG TGTTAACAAT 900
 TTAGTGACCC TTGGTAGGTT AAAGGTTGCA TTATTTATAC TTGAGATTTT TTTCCCCTAA 960
 55 CTATTCGTGTT TTTTGTACTT TAAACTATG GGGGAAATAT CACTGGTCTG TCAAGAAACA 1020
 GCAGTAATTA TTAGTGAGTT AAATTGAAAA GTCCAGTGGA CCAGGCATTT CTTATATAAA 1080
 60 TAAATTTGGT GGTACTAATG TGAAAAAAA AAAAAAAAAA AACTCGAGG GGGCCCGGTA 1140

CCCTATTA

1148

5

(2) INFORMATION FOR SEQ ID NO: 26:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGCACGAGCT AGCTGCCGCC ACCCGAACAG CCTGTCCTGG TGCCCCGGCT CCCTGCCCCG 60
CGCCCCAGTCA TGACCCTGCG CCCCTCACTC CTCCCGCTCC ATCTGCTGCT GCTGCTGCTG 120
20 CTCAGTGCGG CGGTGTGCCG GGCTGAGGCT GGGCTCGAAA CCGAAAGTCC CGTCCGGACC 180
CTCCAAGTGG AGACCCTGGT GGAGCCCCCA GAACCATGTG CCGAGCCCCG TGCTTTTGGA 240
25 GACACGCTTC ACATACACTA CACGGAAGC TTGGTAGATG GACGTATTAT TGACACCTCC 300
CTGACCAGAG ACCCTCTGGT TATAGAACTT GGCCAAAAGC AGGTGATTCC AGGTCTGGAG 360
CAGAGTCTTC TCGACATGTG TGTGGGAGAG AAGCGAAGGG CAATCATTTCC TTCTCACTTG 420
30 GCCTATGGAA AACGGGGATT TCCACCATCT GTCCCAGCGG ATGCAGTGGT GCAGTATGAC 480
GTGGAGCTGA TTGCACTAAT CCGAGCCAAC TACTGGCTAA AGCTGGTGAA GGGCATTTTG 540
35 CCTCTGGTAG GGATGGCCAT GGTGCCAGCC CTCCTGGGCC TCATTGGGTA TCACCTATAC 600
AGAAAGGCCA ATAGACCCAA AGTCTCCAAA AAGAAGCTCA AGGAAGAGAA ACGAAACAAG 660
AGCAAAAAGA AATAATAAAT AATAAATTTT AAAAAAAAAA AAAAAAAAAA AAAAAAA 717
40

45 (2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1099 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GGCACGAGCC GATGTGGACA TCATCCTGTC TATCCCCATG TTCCTGCGCC TGTACCTGAT 60
55 CGCCCGAGTC ATGCTGCTGC ACAGCAAGCT CTTACCGAT GCCTCGTCCC GCAGCATCGG 120
GGCCCTCAAC AAGATCAACT TCAACACCCG CTTTGTGTCATG AAGACGCTCA TGACCATCTG 180
60 CCCTGGCACT GTGCTGCTCG TGTTAGCAT CTCTCTGTGG ATCATTGCTG CCTGGACCGT 240

	CCGTGTCTGT GAAAGTCCTG AATCACCAGC CCAGCCTTCT GGCTCATCAC TTCCTGCTTG	300
	GTACCATGAC CAGCAGGACG TAACTAGTAA CTTTCTGGGT GCCATGTGGC TCATCTCCAT	360
5	CACATTCTTT TCCATTGGTT ATGGGGACAT GGTGCCCCAC ACATACTGTG GGAAAGGTGT	420
	CTGTCTCCTC ACTGGCATCA TGGGTGCAGG CTGCACTGCC CTTGTGGTGG CCGTGGTGGC	480
10	CCGAAAGCTG GAACTACCA AAGCGGAGAA GCACGTTTAT AACTTCATGA TGGACACTCA	540
	GCTCACCAAG CGGATCAAGA ATGCTGCAGC CAATGTCCTT CGGGAAACAT GGTTAATCTA	600
	TAAACACACA AAGCTGCTAA AGAAGATTGA CCATGCCAAA GTGAGGAAAC ACCAGAGGAA	660
15	GTTCTCTCCA AGCTATCCAC CAGTTTGAGG AGCGTCCCAG ATGGAACAGA GGAAAGCTGA	720
	GTGACCAAGC CAACACTCTG GTGGACCTTT CCAAGATGCA GAATGTCATG TATGACTTAA	780
20	TCACAGAACT CAATGACCGG AGCGAAGACC TGGAGAAGCA GATTGGCAGC CTGGAGTCGA	840
	AGCTGGAGCA TCTACCGCC AGCTTCAACT CCCTGCCGCT GCTCATCGCC GACACCCTGC	900
	GCCAGCAGCA GCAGCAGCTC CTGTCTGCCA TCATCGAGGC CCGGGGTGTC AGCGTGGCAG	960
25	TGGGCACCAC CCACACCCCA ATCTCCGATA GCCCCATTGG GGTGAGCTCC ACCTCCTTCC	1020
	CGACCCCGTN CACAAGTTCA AGCAGTTGCT AAATAAATCT CCCCCTCCA GAAGCATTA	1080
30	AAAAAAAAA AAAAAAAAAA	1099

35 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

45	AATTGCGCAG AGAGCCAACC GAGGGCGTTC CTGTCGGGGC TGCAGCGGCG GGAGGGAGCC	60
	CAGTGGAGGC GCCCTCCCGA AGCGCCACTG CCCATGCTGA CCACCCAGCC CTCCGGCTGC	120
	TGATGTCATG AGTAACACCA CTGTGCCCAA TGCCCCCAG GCCAACAGCG ACTCCATGGT	180
50	GGGCTATGTG TTGGGGCCCT TCTTCCTCAT CACCCTGGTC GGGGTGGTGG TGGCTGTGGT	240
	AATGTATGTA CAGAAGAAAA AGCGGTGGA CCGCTGCGC CATCACCTGC TCCCCATGTA	300
55	CAGCTATGAC CCAGCTGAGG AACTGCATGA GGCTGAGCAG GAGCTGCTCT CTGACATGGG	360
	AGACCCCAAG GTGGTACATG GCTGGCAGAG TGGCTACCAG CACAAGCGGA TGCCACTGCT	420
60	GGATGTCAAG ACGTGACCTG ACCCCCTTGC CCCACCCTTC AGAGCCTGGG GTYCTGGACT	480

GCCTGGGGCC CTGCCATCTG CTTCCCCTGC TGTCACCTGG STCCCCCTGC TGGGTGCTGG 540
 GTCTCCATTT CTCCCTCCAC CCACCCTCAG CAGCATCTGC TTCCCATGCC CTCACCATCA 600
 5 CCTCACTGCC CCCAGGCCTT CTGCCCTTTG TGGGTGTTGA GCTCACCGCC CACCCACAGG 660
 CACTCATGGG AAGAGGCTTT CCTTCTGGGA TGGCGGCGGC TGGTAGACAC CTTTGCTTTC 720
 10 TCTAGCCCTC CTGGGCTGGG CTTGGGCACA AATCCCCAGG CAGGCTTTGG AGTTGTTTCC 780
 ATGGTGATGG GGCCAGATGT ATAGTATTCA GTATATATTT TGTAAATAAA ATGTTTTGTG 840
 GCTAAAAAAA AAAAAAAAAA ATCNAAGGGG GGGCCGGTAC CCAAATTCCC CCTATANTGA 900
 15 ATTCGTATTA ACAATTCACT TGGGGCCGTC CTTTAAANAA C 941

20 (2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

30 GGCACGAGGA AGCTGGAGCG GGCCGGCGGT GCAGTCACGG GGGAGCGAGG CCTGCTGGGC 60
 TTGGCAACGA GGGACTCGGC CTCGGAGGCG ACCCAGACCA CACAGACACT GGGTCAAGGA 120
 35 GTAAGCAGAG GATAACAAC TGGAAGGAGA GCAAGCACAA AGTCATCATG GCTTCAGCGT 180
 CTGCTCGTGG AAACCAAGAT AAAGATGCCC ATTTTCCACC ACCAAGCAAG CAGAGCCTGT 240
 TGTTTTGTCC AAAATCAAAA CTGCACATCC ACAGAGCAGA GATCTCAAAG ATTATGCGAG 300
 40 AATGTCAGGA AGAAAGTTTC TGGAAGAGAG CTCCTGCCTTT TTCTCTTGTA AGCATGCTTG 360
 TCACCCAGGG ACTAGTCTAC CAAGGTATT TGGCAGCTAA TTCTAGATTT GGATCATTGC 420
 45 CCAAAGTTGC ACTTGCTGGT CTCTTGGGAT TTGGCCTTGG AAAGGTATCA TACATAGGAG 480
 TATGCCAGAG TAAATTCCAT TTTTGTGAAG ATCAGCTCCG TGGGGCTGGT TTTGGTCCAC 540
 AGCATAACAG GCACTGCCCTC CTTACCTGTG AGGAATGCAA AATAAAGCAT GGATTAAGTG 600
 50 AGAAGGGAGA CTCTCAGCCT TCAGCTTCCT AAATCTGTG TCTGTGACTT TCGAAGTTT 660
 TTAAACCTCT GAATTTGTAC ACATTTAAAA TTTCAAGTGT ACTTTAAAT AAAATACTTC 720
 55 TAATGGAAAA AAAAAAAAAA AAAAAAAAAA ACTCGA 756

60 (2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

5	NCCAGAGGCA GAAAGTCCTG CTTCTGGGGC GTAACCTACA GGATATCCTT GGAACAGAAG	60
10	ATCTTATTGT GGAAGTRACT TCCAATGATG CTGTGAGATT TTATCCCTGG ACCATTGATA	120
	ATAAATACTA TTCAGCAGAC ATCAATCTAT GTGTGGTGCC AAACAAATTT CTTGTTACTG	180
15	CAGAGATTGC AGAATCTGTC CAAGCATTTG TGGTTTACTT TGACAGCACA CAAAATCGG	240
	GCCTTGATAG TGTCTCCTCA TGGCTTCCAC TGGCAAAAGC ATGGTTACCY GAGGTGATGA	300
20	TCTTGGTCTG CGATAGAGTG TCTGAAGATG GTATAAACCG AAAAAAGCT CAAGAATGGT	360
	GCATCCAAAC ATGGCTTTGA ATTGGTAGAA CTTAGTCCAG AGGAGTTGCC TGAGGAGGAT	420
	GATGACTTCC CAGAATCTAC AGGAGTAAAG CGAATTGTCC AAGCCCTGAA TGCCAATGTG	480
25	TGGTCCAATG TAGTGATGAA GAATGATAGG AACCAAGGCT TTAGCTTGCT GCAACTCATT	540
	GACTGGAACA AACCATAGCA TTGGGTCAGC AGATCCCTGT CACCCAGAGC AACCCCATTT	600
30	GCCAGCAGCA GATAGTACTG AATCCCTCTC TGATCATCGG GGTGGTGCAT CTAACACAAC	660
	AGATGCCCAG GTTGATAGCA TTGTGGATCC CATGTTAGAT CTGGATATTC AAGAATTAGC	720
	CAGTCTTACC ACTGGAGGAG GAGATGTGGA GAATTTTGAA AGACTCTTTT CAAAGTTAAA	780
35	GGAAATGAAA GACAAGGCTG CGACGCTTCC TCATGAGCAA AGAAAAGTGC ATGCAGAAAA	840
	GGTGGCCAAA GCATTCTGGA TGGCAATCGG GGGAGACAGA GATGAAATTG AAGGCCTTTC	900
40	ATCTGATGAA GAGCACTGAA TTATTCATAC TAGGGTTTGA CCAACAAAGA TGCTAGCTGT	960
	CTCTGAGATA CCTCTCTACT CAGCCCAGTC ATATTTTGCC AAAATTGCCC TTATCATGTT	1020
	GGCTGCCTGA CTGTGTTATA GGGTCCCCTT AATTTTAGTT TTTAGTAGGA GGTAAAGGAG	1080
45	AAATCTTTTT TTTCCTCAGT ATATTGTAAG AGAGTGAGGA ATACAGTGAT AGTAATGAGT	1140
	GAGGATTTCT TAAATRTACT TTTTTTTTGT TCTAGGAATG AGGGTAGGAT AAATCTCAGA	1200
50	GGTCTGTGTG ATTTACTCAA GTTGAAGACA ACCTCCAGGC CATTCCTGGT CAACCTTTTA	1260
	AGTAGCATTT CCAGCATTC AACTTGATAC TGCACATCAG GAGTTGTGTC ACCTTTCCTG	1320
	GGTGATTTGG GTTTTCTCCA TTCAAGGAGC TTGTAGCTCT GAAGCTATGA TGCTTTTATT	1380
55	GGGAGGAAAG GAGGCAGCTG CAGAATTGAT GTGAGCTATG TGGGGCCGAA GTCTCAGCCC	1440
	GCAGCTAAGT CTCTACCTAA GAAAATGCCT CTGGGCATTC TTTTGAAGTA TAGTGTCTGA	1500
60	GCTCATGCTA GAAAGAATCA AAAAGCCAGT GTGGATTTTT AGACTGTAAT AAATGAGGCA	1560

AAGGATTTCT ATTCCAGTGG GAAGRAAACC TCTCTACTGA GTTGTGGGGG ATATGTTGTA 1620
 TGTTAGAGAG AACCTTAAGG AGTCCTTGTA TGGGCCATGG AGACAGTATG TGATAACATA 1680
 5 CCGTGATTTT CATGAAGAAA TTCTTCTGTC TTAGAGTTCT CCCCTGCTGC TTGAGATGCC 1740
 AGAGCTGTGT TGTTCACAC CTGCAAAACA AGGCACATTT CCCCCTTTCT CTTTAAAGCC 1800
 AAAGAGAGAT CACTGCCAAA GTGGGAGCAC TAAGGGGTGG GTGGGGAAGT GAAATGTTAG 1860
 10 GCGATGAATT CCTGAGCACC TTGTTTTTCT TCCAAGGTTC GTAGCTCCTC TCTGCCCTTC 1920
 CAAGCCTGTA ACCTCGGAGG ACTATCTTTT GTTCTTTATC CTTTGTCTTG TTTGAGTGGG 1980
 15 TCAGCCCCAG AGGAAC TGAT AAGCAAATGG CAAGTTTATA AAGGAAGAGT GGAAAGTACT 2040
 GCAAATAAAA ATCCTTATTT GTTTTGTAG AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2100

20

(2) INFORMATION FOR SEQ ID NO: 31:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AAAAAAAAAA AAAGCCCACC TGAAAGCCTG TCTCTTTCCA CTTTGTGGC CCTTCCAGTG 60
 GGATTATCGA GCATGTTGTT TTTTCATAGT GCCTTTTTTC TTATTTCAAG GGTGCTTCT 120
 35 GAGTGGTGTT TTTTTTTTTT TTAATTGTT TTGTTTAA ATAAGTTAA GACAGTCCAG 180
 AGCTTTTCAG CCAATTTGTC TCCTACTCTG TGTAATATTT TTTCCCTCCG GGCAGGGGAG 240
 40 CCAGGGTAGA GCAAAGGAGA CAAGCAGGAG TGGAAGGTGA GCGTTCTCC TGCTTGACT 300
 AAGCCAGGAG STTTAAGCTC CAGCTTTAAG GGTGTGAGC CCCTTGGGGT TCAGGGAAC 360
 GCTTGCCAG GGTGCACTGT GAGTGTGATG GGCCACCGG GCAAGAGGGA AGGTGACCGC 420
 45 CCAGCTCTCC CACATCCCAC TGGATCTGGC TTACAGGGGG GTCGGAAGCC TGTCTCACC 480
 GTCTCGGGGG TTGTGGCCCC CGCCCCCTCC CTATATGCAC CCCTGGAACC AGCAAGTCCC 540
 50 AGACAAGGAG AGCGGAGGAG GAAGTCATGG GAACGCAGCC TCCAGTTGTA GCAGGTTTCA 600
 CTATTCCTAT GCTGGGGTAC ACAGTGAGAG TACTCACTTT TCACTTGTCT TGCTCTTAGA 660
 TTGGGCCATG GCTTTCATCC TGTGTCCCT GACCTGTCCA GGTGAGTGTG AGGGCAGCAC 720
 55 TGGGAAGCTG GAGTGTGCT TGTGCCTCCC TTCCAGTGG GCTGTGTTGA CTGCTGCTCC 780
 CCACCCCTAC CGATGGTCCC AGGAAGCAGG GAGAGTTGGG GAAGGCAAGA TTGGAAAGAC 840
 60 AGGAAGACCA AGGCCTCGGC AGAACTCTCT GTCTTCTCTC CACTTCTGGT CCCCTGTGGT 900

5 GATGTGCCTG TAATCTTTTT CTCCACCCAA ACCCCTTCCC ACGACAAAA CAAGACTGCC 960
 TCCCTCTCTT CCGGGAGCTG GTGACAGCCT TGGGCCTTTC AGTCCCAAAG CGGCCGATGG 1020
 GAGTCTCCCT CCGACTCCAG ATATGAACAG GGCCAGGCC TGGAGCGTTT GCTGTGCCAG 1080
 GAGGCGGCAG CTC'TCTGGG CAGAGCCTGT CCCC GCCTTC CCTCACTCTT CCTCATCCTG 1140
 10 CTTCTCTTTT CCTCGCAGAT GATAAAAGGA ATCTGGCATT CTACACCTGG ACCATTTGAT 1200
 TGT'TTATTT TGAATTGGT GTATATCATG AAGCCTTGCT GAACTAAGTT TTGTGTGTAT 1260
 ATATTTAAAA AAAAAATCAG TGT'TTAAATA AAGACCTATG TACTTAATCC TTTAAC'TCTG 1320
 15 CGGATAGCAT TTGGTAGGTA GTGATTA'ACT GTGAATAATA AATACACAAT GAATTCTTMA 1380
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAACCCCGGG GGGGGCCCCG GGCCCCAATT 1440
 20 CCCCCCAA 1448

25 (2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 456 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

35 GGCACAGCAA ACTTGACGCC ATGAAGATCC CGGTCC'TTCC TGCCGTGGTG CTCCTCTCCC 60
 TCCTGGTGTCT CCACTCTGCC CAGGGAGCCA CCCTGGGTGG TCCTGAGGAA GAAAGCACCA 120
 TTGAGAATTA TGCGTCACGA CCCGAGGCCT TTAACACCCC GTTCCTGAAC ATCGACAAAT 180
 40 TGCGATCTGC GTTTAAGGCT GATGAGTTCC TGA'ACTGGCA CGCCCTCTTT GAGTCTATCA 240
 AAAGGAACT TCCTTTCCTC AACTGGGATG CCTTTCCTAA GCTGAAAGGA CTGAGGAGCG 300
 45 CAACTCCTGA TGCCCA'GTGA CCATGACCTC CACTGGAAGA GGGGGCTAGC GTGAGCGCTG 360
 ATTCTCAACC TACCATAACT CTTTCCTGCC TCAGGA'ACTC CAATAAAACA TTTTCCATCC 420
 AAAAAAAAAA AAAAAAAAC CCCNGGGGGG GCCCGG 456
 50

(2) INFORMATION FOR SEQ ID NO: 33:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

5	GGCACGAGTG CAGGCCCAGA GAGGACTCAT TGAAAGGACT GAAAGGGGAG GTGGCGTTTT	60
	CTTCCTACCC AAACCTACCC CTGTGAGCTG GACAGCTTGG TAGCACCTGC CTGGACTTAG	120
	ATGGTGGTAG CCAAGAAGAC TGACATTTTA GGAACAGGA CGGGGAGGAG AAGGCTCTGG	180
10	CACACACACA TGTGTCCATA TGTCTGCAA TGGTCTGGG ACTATTGCTA GGCTAGGAGC	240
	CCTAAGTGTC TTCTTCCTCA TGTCTMTTCT CCCCTGTSTC ATGGGCCCTA AGTCTCTTT	300
	CACTGGGCCT GCCTCAATGA ACGTGCTGCC CAGCTACCCC GAAACACGGC ANCTGCCGGC	360
15	TATCAATGCC CCAGCTGCAA TGGCCCATCT TCCCCAACC AACCTGGCTG GGCCCGTGGG	420
	CTCCGCACTG AGARARAAAS TTGGCACART CAACTGGGCC CGGGCAGGAC TGGGCCYCCC	480
20	TCTGATCGAT GAAGKTGGTG ARCCAGAGC CCGAGCCCCT CAACACGTCT GACTTCTCTG	540
	ACTGGTCTAG TTTTAATGCC AGCAGTACCC CTGGACCAGA GGAGGTAGAC AGCGCCTCTG	600
	CTGCCCCAGC CTCTACAGC CGAGCCCCC GGCCCCCAGC TTCCCCAGGC CGCCCCGAGC	660
25	AGCACACAGT GATCCACATG GGCAATCCTG AGCCCTTGAC TCACGCCCCCT AGGAAGGTGT	720
	ATGATACGCG GGATGATGAC CGGACACCAG GCCTCCATGG AGACTGTGAC GATGACAAGT	780
30	ACCGACGTCG GCCGGCCTTG GGTGGCTGG CCCGGCTGCT AAGGAGCCGG GCTGGGTCTC	840
	GGAAGCGRCC GCTGACCTG CTCCAGCGGG CGGGGCTGCT GCTACTCTTG GACTGCTGG	900
	GCTTCCTGGC CCTCCTTGCC CTCATGTCTC GCCTAGGCCG GGCCGCAGCT GACAGCGATC	960
35	CCAACCTGGA CCCACTCATG AACCTCACA TCCGCGTGGG CCCCTCCTGA GCCCCCTTGC	1020
	TTGTGGCTAG GCCAGCCTAG GATGTGGGTT CTGTGGAGGA GAGGCGGGGT AATGGGGAGG	1080
40	CTGAGGGCAC CTCTTCACTG CCCCTCTCCC TCAAGCCTAA GACACTAAGA CCCAGACCC	1140
	AAAGCCAAGT CCACCAGAGT GGCTGCAGGC CAGGCCTGGA GTCCCCGTGG GTCAAGCATT	1200
	TGTCTTGACT TGCTTTCTC CCGGGTYTCC AGCCTCCGAC CCCTCGCCCC ATGAAGGAGC	1260
45	TGGCAGGTGG AAATAAACAA CAACTTTATT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1320
	AAANAA	1326
50		

(2) INFORMATION FOR SEQ ID NO: 34:

55	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 710 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
60	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

	GCGAAAGAGA AAAAGGCTGG AGCTCCCGCC CCCGGGGCTG TCAGATGGCT TGGGTTTCTG	60
5	CGACGCGATT GGCTCGCGGA GGGCAGAAAT TACTCAGCAA ACATGACTAT TATTAGCTGC	120
	TTAGCAACAG CTCACCAAAG TAGAGAGACC ACCCAGGTAG GCAACCCAGT GTGTGCATCC	180
10	TCGGCTTCGG GGCAGCCTCT GAGAGCGCCA ACCTTCTCGC ATGCAATACT TCCATTAAGG	240
	AATGCTCCCC CTCCTTTCTC TCTTATTCCT TTTCTTTTCA ACAGTGTCTT CTTTGTGTGG	300
	GATGCCCTTTG CGCGCACACA CGCGCGCGCA SGCACACACA CGAACATTTG CCTCGCGGTA	360
15	GACACGGGGG GAAATGTWAT ATTTMTTTTAA GCGCTTAAAC AATTTCTGAA ATTCCTCAAA	420
	GAAAAGCCTT TCAGARGCAC CTTGGCCTCA AGCTGCAACA AATACTGGGA RGTCCGGCTC	480
20	GCATTCCCAG GCCTGCACCA ATAATGACAG CGTGCTGGAT ARTGCGCCAG TGTGTGCCAG	540
	ATTTMTTTTTT CCTCTTCTCT TTTCTTTTAT AACTAAAGGG AAGACTTAGG CTCMTGCAGG	600
	GAACAACGCC TCGCATTAAG ATAAACAGAA TGGAAAGTTA AAGAGGAAAG CAAGGACGTT	660
25	GGGAAAAGCC ATCTTTCTTA AAATCCGTCT GCCCCCAGC CGCTTTCTCC	710

30 (2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|-----------------------------|
| | (A) LENGTH: 1188 base pairs |
| | (B) TYPE: nucleic acid |
| 35 | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

40	GATGGCTTTT ATATCTATTA TCGACCCACA GACAGTGACA ATGATAGTGA CTACAAGAAG	60
	GATATGGTGG AAGGGGACAA GTACTGGCAC TCCATCAGCC ACCTGCAGCC AGAGACCTCC	120
45	TACGACATTA AGATGCAGTG CTTCAATGAA GGAGGGGAGA GCGAGTTCAG CAACGTGATG	180
	ATCTGTGAGA CCAAAGCTCG GAAGTCTTCT GGCCAGCCTG GTCGACTGCC ACCCCCAACT	240
	CTGGCCCCAC CACAGCCGCC CTTCTCTGAA ACCATAGAGC GGCCGGTGGG CACTGGGGCC	300
50	ATGGTGCTC GCTCCAGCGA CTTGCCCTAT CTGATTGTCG GGGTCGTCCT GGGCTCCATC	360
	GTTCTCATCA TCGTCACCTT CATCCCCTTC TGCTTGTGGA GGCCTGGTC TAAGCAAAAA	420
55	CATACAACAG ACCTGGGTTT TCCTCGAAGT GCCCTTCCAC CCTCCTGCCC GTATACTATG	480
	GTGCCATTGG GAGGACTCCC AGGCCACCAG GCAGTGACCA GCCCTACCTC AGTGGCATCA	540
	GTGGACGGGC CTGTGCTAAT GGGATCCACA TGAATAGGGG CTGCCCCTCG GCTGCAGTGG	600
60	GCTACCCGGG CATGAAGCCC CAGCAGCACT GCCCAGCGA GCTTCAGCAG CAGAGTGACA	660

CCAGCAGCCT GCTGAGGCAG ACCCATCTTG GCAATGGATA TGACCCCAA AGTCACCAGA 720
 TCACGAGGGG TCCCAAGTCT AGCCCGGACG AGGGCTCTTT CTTATACACA CTGCCCGACG 780
 5 ACTCCACTCA CCAGCTGCTG CAGCCCCATC ACGACTGCTG CCAACGCCAG GAGCAGCCTG 840
 CTGSTGTGGG CCAGTCAGGG GTGAGGAGAG CCCCCGACAG TCCTGTCCTG GAAGCAGTGT 900
 10 GGGACCCTCC ATTTCACTCA GGGCCCCCAT GCTGCTTGGG CCTTGTGCCA GTTGAAGAGG 960
 TGGACAGTCC TGACTCCTGC CAAGTGAGTG GAGGAGACTG GTGTCCCAG CACCCCGTAG 1020
 GGGCCTACGT AGGACAGGAA CCTGGAATGC AGCTCTCCCC GGGGCCACTG GTGCGTGTGT 1080
 15 CTTTGTAAAC ACCACCTCTC ACAATTTAGG CAGAAGCTGA TATCCCAGAA AGACTATATA 1140
 TTGTTTTTTT TTTAAAAAA AAAAAAAAAA AWCYCGGGG GGGGCCCC 1188
 20

(2) INFORMATION FOR SEQ ID NO: 36:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 956 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGCAGAGCAG TGAATATGCA TCCTAAAAAT TCAATGTTTA TACCAGGCTC ATGACACTAA 60
 35 GATGTGACAT CTGGACACGA GGGGTGAGCC ACGTGGATAC ATCCCTCCCA GATTGCATCT 120
 CCAGGAATCA CTCGTCTAGC AGAATGGGCG CCCCATCCCT TACTATGCTG CTCCTCCTCA 180
 AAGTGCAGCC CAGAAGGACC CAGGCCTTTG ATGCACATTG GGTGGGTCTC CCACTACTTT 240
 40 AGTTGAAATG GGAGCATGCT GGAGTCGGCG TTCTGTTGCT TCTGGTGAGA AGGACATCCC 300
 ATTGACCCCT GGCCACCAGG TCCAGTATTC CATCTTCCT TCTGTCCCAG CCTATCGCCC 360
 45 TCCCCACYAG GCCCAGCCCC ACAACTTCTC CTCAAGGAG GTTNTCCCGC AGCTGGAGGG 420
 CTTGCACAGA CCAGCAGTCA CAGAAATCAT TCTTCTGCT GTACTGGGCC TTAAGTGCCT 480
 GCAATGTCC GAGCACTACT GCATAGGATG CCAGAGCCAC CGAAGATAAA CACAGCCAAG 540
 50 TTTAATAATA ATAAAAGGAA AAATCTCAGC CTGCAGAACT CTGGTTTGA CCCACCATCG 600
 GCCAGATGCA CATCTTCAGG GCCTGTTGAG CACCTTCTGA AAAGCAGGGC TCGTAATAGA 660
 55 CTCCAGCACA TTCCATCAGA GTCAGGAAAA CTGCGGTGAG TCCCAGAGAA TCTAGGGTGC 720
 AGGGCAGGGA GCAGGAGTCA TAAGGAGTGA TAACCTAAAC TGTGTGTAGT CAGCGGGGAG 780
 GGTCTTATGT TATCAGGTGA AATGAGAGCC AGTAAGTTAG TTGATCCTGT CACAGATATA 840
 60

ACCCTGATAA CACCCCATAG ATACGCGACA CGTGTGTCCT GCCCCTGCTT TCCCCATCCA 900
 ACATGGTTCT TCTGTTCCAC AGACATTAAA GGGGCTTTCT GCAATTACTT AAAAAA 956

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(2) INFORMATION FOR SEQ ID NO: 37:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1603 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TCGACCCACG CGTCCGCTCT GCCAGGAATC TGGTCTTTCT GTAGACCCAA GTCAGAAAGA 60
 20 ACCATTGTGT GAGTTAAATC GAATATTAGA RGCATTAAAR GTCAGAGTTC TGAGACCTGC 120
 TCTGGAATGG GCAGTTTCAA ACCGAGAGAT GCTTATAGCC CAAAACAGCT CCTTGGAATT 180
 25 TAAACTACAC AGACTGTATT TTATTAGCTT RTTAATGGGT GGAACACAAA TCAGCGAGAR 240
 GCATTACAAT ATGCTAAAAA TTTTCAGCCA TTTGCCCTAA ATCATCAAAA AGACATTCAG 300
 GTTTTGATGG GAAGCCTTGT GTACCTGAGA CAAGGGATTG AGAACTCACC ATATGTTTAC 360
 30 CTACTTGATG CAAACCAGTG GGCTGATATC TGTGACATCT TTACACGGGA TGCTTGTGCC 420
 CTCCTGGGGC TCTCCGTGGA GTCCCTCTC AGTGTCAGTT TCTCAGCAGG TTGTGTGGCG 480
 CTGCCAGCTT TAATTAAAT CAAAGCCGTG ATTGAACAGA GGCAGTGTAC TGGAGTTTGG 540
 35 AACCAGAAAG ATGAATTACC TATTGAAGTG GACCTTGGTA AAAAGTGCTG GTATCACTCT 600
 ATATTTGCCT GCCCATTTCT TCGTCAGCAA ACAACAGATA ACAATCCACC CATGAAATTG 660
 40 GTCTGTGGTC ATATTATATC AAGAGATGCC CTGAATAAAA TGTTTAATGG TAGCAAATTA 720
 AAATGTCCCT ACTGTCCAAT GGAACAAAGT CCAGGAGATG CCAAACAGAT ATTTTCTCTGA 780
 45 AGAGATAACT TTAGTTTGCA ATTTGTAAGT GAACTGAAT CGTGGGTGCA TTTCAGAAGA 840
 GAACGTTCCA TATAATGCAG CTAACCAAGG ACTCCTGTGT TTCTATAAGC TAATGCTCCA 900
 GAACTTTGC CAACCTGTTA GTGTACACAC ACTGAGGGGA GTGCTCCCGG TGAATATTAT 960
 50 CATAGGGCTT TATTATATTC TTGGTCTTCA TTTCTGATCA AGTAAATACA CCAGCAGTTG 1020
 TCATTCAATG CAGGTTTTTG TACTTAATTA TATGGTGATT TTTTACTTT TTAAGAGCAG 1080
 55 AAACGAAAT TGACCTCCCC GCCATGTGTT TAATATTCCT CCTGCTTTTA CTTTGTTCAT 1140
 TTTCTGATA ATCGTAAGCC TTGAGAGTGT TTGTGAAAAA GTTTTATTTC CTGTTATGTA 1200
 TACATAATTA AATGAAAAAT CTTCAGAAAA AGTTTGATAA ATTGAATTGT GCTTATGAAA 1260
 60 CTAATTTGCA TTTTATTTG CTTAAGAAAG AAAGCTGTGA TAGATTCCAG ATATGCTTTT 1320

	TGATGTTTTTC CTCTGCTCCA GCTCCAAGAA GTCAGCACAC CTGCATTTTA GCTCTGCATG	1380
	CAGCCCCAGC AGGCTGCGTG TTTAAGAATT TCATTGTTTA ACTGGCTGGT GTGAGAAGTC	1440
5	TTCCGTTAGC ATAGAGTGGG AGGAGTACTA TTGTTTGGTT GGGTTTTTGT TTGTTTGTMT	1500
	TTTGTTTTTG CTTTTATTGC CAAGAGGTGC TTGTTTTTAA AGTATGTTTA ATAAAATGAA	1560
10	ATTCTAAAGT TAARAAGTGT TCTTAAAGTT GATATTTAAC TCT	1603
15	(2) INFORMATION FOR SEQ ID NO: 38:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1089 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:	
25	GGCACGAGCT ACCTTTCTGC CTGCTTTGCT GGCTGCAACA GCACGAATCT CACGGGCTGT	60
	GCGTGCCCTCA CCACCGTCCC TGCTGAGAAC GCAACCGTGG TTCCTGGAAG ATGCCCCAGT	120
	CCTGGGTGCC AAGAGGCCTT CCTCACTTTC CTCTGTGTGA TGTGTATCTG CAGCCTGATC	180
30	GGTGCCATGG CAAGACACCC TCAGTCATCA TCCTCATCAG GACAGTCAGC CCTGAACTCA	240
	AGTCTTACGC TTTGGGAGTT CTTTTTCTCC TCCCTCGTTT GTTGGGCTTC ATCCCTCCAC	300
35	CCCTCATCTT CGGGGCTGGC ATCGACTCCA CCTGCGTGT CTGGAGCACG TTCTGTGGGG	360
	AGCAAGGCGC CTGCGTCCTC TACGACAATG TGGTCTACCG ATACCTGTAT GTCAGCATCG	420
	CCATCGCGCT CAAATCCTTC GCCTTCATCC TGTACACCAC CACGTGGCAG TGCTGAGGAA	480
40	AAACTATAAA CGCTACATCA AAAACCACGA GGGCGGGCTG AGCACCAGTG AGTTCTTTGC	540
	CTCTACTCTG ACCCTAGACA ACCTGGGGAG GGACCCTGTG CCCGCAAACC AGACACATAG	600
45	GACAAAGTTT ATCTATAACC TGGAAGACCA TGAGTGGTGT GAAAACATGG AGTCCGTTTT	660
	ATAGTGACTA AAGGAGGGCT GAACTCTGTA TTAGTAATCC AAGGGTCATT TTTTCTTAA	720
	AAAAAGAAAA AAAGGTTCCT AAAAAACCA AAATCAGTA CACACACACA GGCACAGATG	780
50	CACACACAG CAGACAGACA CACCGACTTT GTCCTTTTTC TCAGCATCAG AGCCAGACAG	840
	GATTCAGAA T AAGGAGAGAA TGACATCGTG CGGCAGGGTC CTGGAGGCCA CTCGCGCGGC	900
55	TGGGCCACAG AGTCTACTTT GAAGGCACCT CATGGTTTTC AGGATGCTGA CAGCTGCAAG	960
	CAACAGGCAC TGCCAAATTC AGGGAACAGT GGTGGCCAGC TTGGAGGATG GACATTTCTG	1020
60	GATACACATA CACATACAAA ACAGAAAACA TTTTTTAAAA GAAGTTTCCT AAAATAAAAA	1080

AAAAAAAA

1089

5

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 629 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

15

AGCTCAGTTC CCTTAGAAAT GAAATTTTAA ATGACACTAC CAGGTAAGCC ACTGAGACCA 60

GTGGAGGTGA TAGCTAAGAA CATAAGGAAT TAAGAATTTT TAATGGAGAA AGGAGGTAAT 120

20

GAATACCACT TACATCCTAA GACTCACTGT AGTGGTGAGT GTTGTAATTT ATCTCGCTAT 180

CCATCCTCTT TTAAGTTTTT CCTTAGAAAG TCCTCTATTG GTACCTTGA GGGACTGCTG 240

25

TCAAAATATA TGGAAAAGTG GGTCTGTGTG GTACAAGAGG TGGACTTTGC CACACATGGA 300

AGTTTGCTGC CAAGATCTTC ACTAATGAAA GAAATCACCA GTGAGCTGCA CAGATTAGCC 360

AAATACTGAG CTCATTAGAA CTAATAAGGC CTGGACATTT CTGCCTAATC CAGGACTCCT 420

30

GTAATTATCA GTCTTTGCTT TGGAGCTTCC CATTTGTGTAG CTGARAATTT GTCATATCTG 480

CATTATAATC TAAGGCTCCA CATACTTAAT CCTGCTTCTC CCCCTTTTTC TTTCCCTTTC 540

35

CCAGCGGTCA GCTCTGCTGC ATAGTCTGAA GACTTTCCCT GCCCAATCCT GATAAAATTC 600

TTGCACTCGT AACCCCATCT CAGTGTCTG 629

40

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 1964 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

50

AAGAAGACAT GGAAATTGCT GAAGGATGTT TCAGGCATAT TAAGAAAATC TTTACGCAGC 60

TTGAGGAATT CAGAGCCTCT GAATTGCTTC GAAGTGGACT GGACAGATCT AAATACCTTT 120

55

TAGTGAAAGA AGCCAAAATT ATTGCTATGA CCTGTACTCA TGCTGCCTTA AAACGACATG 180

ACTTGGTCAA GCTAGGTTTC AAGTATGACA ACATTTTGAT GGAAGAGGCT GCTCAGATTTC 240

60

TGGAGATAGA AACTTTTATC CCTCTTCTTC TACAGAATCC TCAGGATGGA TTTAGCCGAC 300

	TAAAACGATG GATTATGATT GGCGATCATC ACCAGTTACC TCCAGTTATT AANGAACATG	360
	GCCTTTCAAA AGTACTCAAA CATGGAGCAG TCTCTCTTCA CTCGCTTTGT TCGCGTTGGA	420
5	GTTCGACTG TTGACCTTGA TGCTCAAGGG AGAGCCAGAG CAAGCTTGTG CAMCTNCTAC	480
	AACTGGCGAT ACAAGAATCT AGGAAACTTA CCCCATGTGC AGCTCTTGCC AGAGTTTAGT	540
10	ACAGCAAATG CTGGCTTACT GTATGACTTC CAGCTCATTA ATGTTGAAGA TTTTCAAGGA	600
	GTGGGAGAAT CTGAACCTAA TCCTTACTTC TATCAGAATC TTGGAGAGGC AGAATATGTA	660
	GTAGCACTTT TTATGTACAT GTGTTTACTT GGTTACCCTG CTGACAAAAT CAGTATTCTA	720
15	ACAACATATA ATGGCCAAAA GCATCTTATT CGCGACATCA TCAATAGACG ATGTGGAAC	780
	AATCCATTGA TTGGAAGACC AAACAAGGTG ACAACTGTTG ATAGATTTCA AGGTCAACAG	840
20	AATGACTATA TTCTTCTTTC TCTGGTACGA ACCAGGGCAG TGGGCCATCT GAGGGATGTC	900
	CGTCGCTTGG TAGTGGCCAT GTCTAGAGCC AGACTTGGAC TTTATATCTT CGCCAGAGTA	960
	TCCCTCTTCC AAAACTGTTT TGAAGTACT CCAGCTTTCA GTCAGCTCAC AGCTCGCCCC	1020
25	CTTCATTGTC ATATAATTCC AACAGAACCT TTCCCAACTA CTAGAAAGAA TGGAGAGAGA	1080
	CCATCTCATG AAGTACAAAT AATAAAAAAT ATGCCCCAGA TGGCAAACCTT TGTATACAAC	1140
30	ATGTACATGC ATTTGATACA GACTACACAT CATTATCATC AGACTTTATT ACAACTACCA	1200
	CCTGCTATGG TAGAAGAGGG TGAGGAAGTT CAAAATCAAG AAACAGAATT GGAAACAGAA	1260
	GAAGAGGCCA TGAAGTTTCA AGCTGACATC ATACCCAGTC CAACAGACAC CAGCTGCCGT	1320
35	CAAGAACTC CAGCCTTTCA AACTGACACC ACCCCAGTG AGACAGGAGC CACTTCCACT	1380
	CCAGAAGCCA TCCCTGCTTT ATCTGAGACC ACCCCTACTG TGGTAGGAGC TGTATCTGCA	1440
40	CCGGCAGAAG CTAACACACC TCAGGATGCC ACATCTGCCC CAGAAGAGAC CAAGTAGCCA	1500
	AACTGTAGTC CTTCTAAAGG AGGACATGGC AGTCAAAAAG TCTGAGTAAA GCTGTTTTTT	1560
	GTATTTTATA TTTGCTTCTG CCATTTTACT GTCATAATT AATGTTTAGT TCTTATATTT	1620
45	GTAACTGAT TTCGGTGTCT TGAATATATT TTTTAAATTT ATGTGTATGA ACAATTCTAG	1680
	TTTCATTTGT TCAATCAGAA GAGCAAATAA CCATTCCTTT CATGTTTTGA TCACTGAGTG	1740
50	TGTCTGTAAT CATACTACA TTAAAATCAT TTTCTATGAA TATATAATAT ATACTTCACA	1800
	TTTTTAGTGA ACTTCTCTAA AGAAGAGGAC AGAATATACT GGACTTAACC ACGAATACCC	1860
	TTGAGTGTCC AAATTGGGAA GGAACKGTT TCTTCYGTTA TACTAYCAAA TGCTTAAATT	1920
55	CKGTTTCCTT TTTTCTTACC TTTGTTTGCT GTCTTTATGT AAAG	1964

60 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

10	CGTGTCCGCG CGCCTGGGAG ACGCTGCCTC GGCCCGGACG CGCCCGCGCC CCCGCGGCTG	60
	GAGGGTGGTC GCCACTGGGA CACTGTGAAC CAGGAGTRAG TCGGAGCTGC CGCGCTGCCC	120
	AGGCCATGGA CTGTGAGGTC AACAAACGGTT CCAGCCTCAG GGATGAGTGC ATCACAAACC	180
15	TACTGGTGT TGGCTTCCTC CAAAGCTGTT CTGACAACAG CTTCCGCAGA GAGCTGGACG	240
	CACTGGGCCA CGAGCTGCCA GTGCTGGCTC CCCAGTGGGA GGGCTACGAT GAGCTGCAGA	300
20	CTGATGGCAA CCGCAGCAGC CACTCCCGCT TGGAAGAAT AGAGGCAGAT TCTGAAAGTC	360
	AAGAAGACAT CATCCGAAT ATTGCCAGGC ACCTCGCCA GGTGCGGGAC AGCATGGACC	420
	GTAGCATCCC TCCGGGCTG GTGAACGGCC TGGCCCTGCA GCTCAGGAAC ACCAGCCGGT	480
25	CGGAGGAGGA CCGGAACAGG GACCTGGCCA CTGCCCTGGA GCAGCTGCTG CAGGCCTACC	540
	CTAGAGACAT GGAGAAGGAG AAGACCATGC TGGTGTGGC CCTGCTGCTG GCCAAGAAGG	600
30	TGGCCAGTCA CACGCCGTCC TTGCTCCGTG ATGTCTTTCA CACAACAGTG AATTTTATTA	660
	ACCAGAACCT ACGCACCTAC GTGAGGAGCT TAGCCAGAAA TGGGATGGAC TGAACGGACA	720
	GTTCCAGAAG TGTGACTGGC TAAAGCTCGA TGTGGTCACA GCTGTATAGC TGCTTCCAGT	780
35	GTAGACGGAG CCCTGGCATG TCAACAGCGT TCCTAGAGAA GACAGGCTGG AAGATAGCTG	840
	TGACTTCTAT TTTAAAGACA ATGTTAACT TATAACCCAC TTTAAAATAT CTACATTAAT	900
40	ATACTTGAAT GAAATGTCC ATTTACACGT ATTTGAATGG CCTTCATATC ATCCACACAT	960
	GAATCTGCAC ATCTGTAAAT CTACACACGG TGCCTTTATT TCCACTGTGC AGGTTCACAC	1020
	TTAAAAATTA AATTGGAAAG CAGGTTTCAA GGAAGTAGAA ACAAATACA ATTTTTTGG	1080
45	TAAAAAATAA TTAAGTACA ACCATAGAGG ATGGTCTTAC AGCAGGCAGT	1140
	ATCCTGTTTG AGGAAAGCAA GAATCAGAGA AGGAACATAC CCCTTACAAA TGAAAAATTC	1200
50	CACTCAAAAT AGGGACTATC YATCTTAATA CTAAGGAACC AACAATCTTC CTGTTTAAAA	1260
	AACCACATGG CACAGAGATT CNGAACTAAA GTGCTGCACT CAAATGATGG GAAGTCCCGG	1320
	CCCCAGTACA CCAGGGGCTT TGGACTTTTT TCAACTTCGT TTCCTTTTGT TTGGANTCCA	1380
55	AAAGAACCAC TTTGTGGTTC TTAAGGGT GTGAAGGTGA TTTAAGGGGC CCAGGTCAGC	1440
	CACTGGTTGG TTTACAAAAT CNGGGTAACT AACTGCATAC AACTTTTTC CTTTCCATG	1500
60	NCATCAGGAC TTGCTAAAG AC	1522

5 (2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 875 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

15 TGGGATTTC CTTTATCATG GAGGCCTTGT CCCACTTCCT CTATGTCCCT TTCCTTGGTG 60
TCTGTGTCTG TGGGGCCATC TACACTGGCC TGTTCCCTCC TGAGACCAAA GGCAAGACCT 120
TCCAAGAGAT CTCCGAGGAA TTACACAGAC TCAACTTCCC CAGGCGGGCC CAGGGCCCCA 180
20 CGTGGAGGAG CCTGGAGGTT ATCCAGTCAA CAGAACTCTA GTCCCAAAGG GGTGGCCGTA 240
GCCAAAGCCA GCTACCGTCC TGTCTCTGTC TTCCTGCCAG GGCCCTGGTC CTCAMTYCCT 300
25 YCTGCATTCC TCATTTAAGG AGTGTATTAT GAGCACCTT TGTGTGCAGA CATGGCTCCA 360
GGTGCCTTAGC AATCAWTGGT GAGCGTGGTA TCCAGGCTAA AGGTAATTAA CTGACAGRAA 420
ATCAGTAACA ACATAATTAC AGGYTGGTTG TGGCAGYTCA TGA CTGTAAT CCCAGCACTT 480
30 TTGGGAGCCA AGGTGGGARG ATCAATTGAG GCCAGAGTTT GAAAMCAGCT AGGTAACATA 540
GTGAGACCCC CTATCTCTAC AAAAAATTTT AAACATTAGC TGGGCATGGT GGTATGTGCT 600
35 AACAGCTCTA GCTACTCAGG AGGCTGAGGC AGCAGGATCA CTTGAGTCCA AGAGTTCAAG 660
GTAGCAGTAA GCTACAATCA CACCACTGCA TGCCAGACTG GGTGACAGAG GGAGACTTCA 720
TCTCTTTAAA ACATAATAAT AATAATTACA GACTCAGGAA ATGCAGTGAA AGAAAAATAC 780
40 AGGTTGGCCA GGTGAGGTGG CTGATGCCTG TAATCCCAGC ACTTTGGGAG GCCAAGATGG 840
GAAGATGCT TTGAGACCAG AAGTTTGAGA CCAGC 875

45

(2) INFORMATION FOR SEQ ID NO: 43:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CCCACGCGGT CCGNATCGTC CTTCCCTCAC TTCAGAGGGT GGCCAGAGCT GAATACCCAG 60
60 AGAGGGACAA GTAAGGGTCC AGTTCCAAAA CATCATGAGG ATGTATCATC CCACGTGTCT 120

5 CACCTGACAG TTACAGAGGA AACCCGCACC CAGAATGCAC GTGCTGTC'TT ATGGGAACAC 180
 TCAGCGCAGA GTGCTCAGGT CCGGCCACAC TCGGGCTGTG CTTGGTCGTG CCATGGAATT 240
 CCTCAGGACT TTCTCAGCCT CCCTAATGGC AGAAGCCCCT TTACAGCAAG ACATTTACCG 300
 TTTGTCTGAA AATAGCCGAA CTGAGCTTTT CTTCAGGCTA TATGAGAAGT CTCTAGACAG 360
 10 TGGGCACCGT CAGAAAGCCC AGAGCCTTGT GATAGCTCCC ACCCTGCCTG GCTCAGATCT 420
 TCCCATTTTT TTTCTCTGG CACTAACCTC ACCTTTTGTT TTTTGTGTT TGTGTTGTT 480
 TTTGTTTTTG CAGAGTTGGA TTACAGAAAC TCCTATGAAA TTGAATATAT GGAGAAAATT 540
 15 GGCTCCTCCT TACCTGTAAG TTCGTCTGCC TCGGGCCACT TAGGGGACTC GCTTTCCTGC 600
 CTTCAGGGGC CTCCTCCCCT GTGCAGAGTG TCTCTGGAG CTCAGACCCC AAATCGAGTG 660
 20 TTTTCTGTGT ACACAGCTTC CCGGGTGCAC AGCAATGATG GACTGGGGCT GGGGGGTTGA 720
 GGTTTGTACT CAATCCACTT CGTTTGACAT TTTCAGGGAG AAAATGATAG AATACAATTA 780
 GACGTCCTGC AGAATPACTT TCCTAGACTG AGAAAGAGCT AGAGATTTCT TTAACAAAAA 840
 25 AAA 843

30

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 489 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

40 CTCTTAGGCT TTGAAGCATT TTTGTCTGTG CTCCCTGATC TTCAGGTCAC CACCATGAAG 60
 TTCTTAGCAG TCCTGGTACT CTTGGGAGTT TCCATCTTTC TGGTCTCTGC CCAGAATCCG 120
 45 ACAACAGCTG CTCCAGCTGA CACGTATCCA GCTACTGGTC CTGCTGATGA TGAAGCCCCT 180
 GATGCTGAAA CCACTGCTGC TGCAACCACT GCGACCACTG CTGCTCCTAC CACTGCAACC 240
 ACCGCTGCTT CTACCACTGC TCGTAAAGAC ATTCCAGTTT TACCCAAATG GGTGGGGAT 300
 50 CTCCCGAATG GTAGAGTGTG TCCCTGAGAT GGAATCAGCT TGAGTCTTCT GCAATTGGTC 360
 ACAACTATTC ATGCTTCCTG TGATTTTCATC CAACTACTTA CCTTGCCTAC GATATCCCCT 420
 55 TTATCTCTAA TCAGTTTATT TTCTTTCAAA TAAAAAATAA CTATGAGCAA CAAAAAATAA 480
 AAAAAAATAA 489

60

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 534 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

10 GAAGCAGTGT GTATCTATGA TTATATCTCT GTTCATCTAT ATATTTTGA CATGTAGCAA 60
 CACCTCTCCA TCTTATCAAG GAACTCAACT CGGTCTGGGT CTCCCCAGTG CCCAGTGGTG 120
 15 GCCTTTGACA GGTAGGAGGA TGCAGTGCTG CAGGCTATTT TGTTTTTTGT TACAAACTG 180
 TCTTTTCCCT TTTCCCTCC ACCTGATTCA GCATGATCCC TGTGAGCTGG TTCTCACAAT 240
 20 CTCTGGGAC TGGGCTGAGG CAGGGGCTTC GCTCTATTCT CCCTAACCAT ACTGCTTCC 300
 TTTCCCTTG CCACTTAGCA GTTATCCCC CAGCTATGCC TTCTCCCTCC CTCCCTTGCC 360
 CTGGCATATA TTGTGCCTTA TTTATGCTGC AAATATAACA TTAACTATC AAGTGAAAAA 420
 25 AAAAAAAAAA AAAACTCCAA GGGGGGGCCG GTACCCAATT CCCCCTATAN TGAGTCNTAT 480
 TACAATTAC TGGGCCGTCG TTTTACAACG TCGTGAATGG GAAACCTGG GCGT 534

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GGCACGAGTC CGGATGAGC TCAGCCGCGG CCGACCACTG GCGTGGTGTG CTGGTGCTCA 60
 45 GCTTCGTGTT TGGATGCAAT GTTCTTAGGA TCCTCCTCCC GTCCTTCTCA TCCTTCATGT 120
 CCAGGGTGCT GCAGAAGGAC GCGGAGCAGG AGTCACAGAT GAGAGCGGAG ATCCAGGACA 180
 TGAAGCAGGA GCTCTCCACA GTCAACATGA TGGACGAGTT TGCCAGATAT GCCAGGCTGG 240
 50 AAAGAAAGAT CAACAAGATG ACGGATAAGC TCAAAACCCA TGTGAAAGCT CGGACAGCTC 300
 AATTAGCCAA GATAAAATGG GTGATAAGTG TCGCTTTCTA CGTATTGCAG GCTGCCCTGA 360
 55 TGATCTCACT CATTTGGAAG TATTATTCTG TCCCTGTGGC TGTCGTGCCG AGTAAATGGA 420
 TAACCCCTCT AGACCGCCTG GTAGCCTTTC CTACTAGAGT AGCAGGTGGT GTTGAATTA 480
 CCTGTTGGAT TTAGTCTGT AACAAAGTTG TCGCTATTGT GCTTCATCCG TTCAGCTGAA 540
 60

200

CAGGAGGATG GATACAGCCG CGAGGCTAAA AAACGGATTT CCTCTTCCTA GCTTAAAATC 600
 TGATTTACAC TGTTTTGT TTAAAGAAAC AAAAGTGCAT AGTTTAGATT TTTT TTTT TG 660
 5 TTGAATATGT TTGTTCTTGG ACTTTATGAG AGAGTCTTAT AAGAATCACG ATTTTCTACA 720
 CCTGTCATTG AGCCAAGAAA GTCCAGTTTA TGACACGTAT GTACTAGTGA ACACCGTCCT 780
 10 CGATCTGTAC GAAATGTGAA ATGTTTAGGG ACATCTCCAT GCTGTCACTT GTGATTTGCC 840
 CTCTTATGTA TTTTGGTCAT ATTGCCAACT GGAAAGTCAA AATTTTCTAA CAACTTTAAG 900
 TAAGTTCTTT GAAGACTTAG TGCTGTTTTT AATCCAGTTT AGAAAGTAAC TTAATTTTAA 960
 15 TACCACTACT AAAAATTCGA AAATTTCTTC TTAAATCACA TTCAATATGG TTAAAAGAAC 1020
 AACACTAATT GACATTGCGT GGGCTTTTTC TCCCTTTGTT TAAAATGTCA TTTGTTGAGC 1080
 AAGAGTTGTA TAGTATTATC TACTTACTTG AGGCTGTAA TTTTTCATTA CAGTGTTTTG 1140
 20 TAAATGTATC CACGAGACCA TGATGCATTG TTTTGTGCTC AACTTGTGTT TTGTATTTAA 1200
 AGCATTTTGA ATGAAGTGTA TTTTATAAGC ATTTAATATT TATGCTCTTT AGAATGGAAC 1260
 25 ACAGAAAACA AACCTTATAA GTCCTGATTA ATCTGAACCA ATAACCTGTG TGGCCTACAA 1320
 AGTATAATTC TATTAAATGT TCCTTAAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1374

30

(2) INFORMATION FOR SEQ ID NO: 47:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GAATTCGNCA CGAGATTACT TGGACATGAA AGAACTCAGG TTCAAGTTTA TTCATTTACT 60
 AAGTTAGTTA AATCATGTGC CTTCCATGAG CCTTCATTTG GTAACCTGGA AAATGGAAAT 120
 45 AATAACACTA GTCATATATA TTCTACACTG CTACCATATG GACCAAAGGG ATTATAGATT 180
 ACAATCACCA TCATTCTGTC TGACAGGTAT ATAGAAAACA ATTTTCATTGA AGAAAAGTCC 240
 50 TTACATTTAT CCTTTTCCTA ATATCTGCAT GGGTAAACTA ATAAATATAG TCATTAGAAA 300
 ACCCTTATTA TTATTATTAG TTCAATGTGA GAACTGCTGC AGAAAAATA TGC'TTATAA 360
 TATTTTCTTG AATATACATA ATATTCATAA ATTTTCAAAT CATTGAAAAT TACCTTAAAA 420
 55 TTGGAAAAAA TGTGCATTTT TACTCATATA ACAGTATAAA ATTCTCTATGT CAATCTCTTT 480
 TTTT TTTT TTTT TGTTTTGAGT TGGAGTCTCG CTCTGTGCGC CAGGCTGGGC AACAGAGCAG 540
 60 GACCCTGTCT TAATTAATAA AAAAAAAAAA AAACTCGAGG GGGGCCCGGT ACCCTA 596

5 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 851 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

15 CACATGAAGA CACACAGTGG TGAGAAGCCC TTCCGCTGCG CCCGCTGTCC TTATGCCTCT 60
CCTCATCTGG ATAACCTGAA ACGGCACCAG CGCGTCCATA CAGGAGAGAA GCCCTACAAG 120
TGCCCCCTCT GCCCTTATGC CTGTGGCAAT CTGGCCAACC TCAAGCGTCA TGGTCGCATC 180
20 CACTCTGGTG ACAAACCTTT TCGGTGTAGC CTTTGCAACT ACAGCTGCAA CCAGAGCATG 240
AACCTCAAAC GTCACATGCT GCGGCACACA GGCAGAGAAGC CTTCCGCTGT GCCACCTGCG 300
25 CCTATACCAC GGGCCACTGG GACAACTACA AGCGCCACCA GAAGGTGCAT GGCCACGGTG 360
GGGCAGGAGG GCCTGGTCTC TCTGCCTCTG AGGGCTGGGC CCCACCTCAT AGCCCAACCCT 420
CTGTTTTGAG CTCTCGGGGC CCACCAGCCC TGGGGACTGC TGGCAGCCGG GCTGTCCACA 480
30 CAGACTCATC CTGAACTAGG TCCTTCTTCC CCATGTTTTA TACAGACGGA CCAGAAGCCA 540
CCTTTTTCTC CCCCCTGGC CAGGGGCTCC ACACAGACTA ACGTAGGCAC TATAAGGACC 600
35 AGCCCAACCC CATGGGCGGG GGGGCCCATTA TGGACCAGGG GACCTTGCCT TGAAGTGGC 660
ACTTCACGAG CTCAGTGAGA AGGGCCCTGT ATTACCTCC ACTGCCCCCA GGGGCTGTGG 720
ACAAACCGGC TGGGGGACTG CCCAGCCTCC CACCTGTTTA TTAACTTAT TTCAGTGCTT 780
40 TATAATAAAG GAAACACTAA CAAAGCCATG TCTATGCTGA ATTGGCAATG GCAGGCAATT 840
TGGCCTTACC C 851

45

(2) INFORMATION FOR SEQ ID NO: 49:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GTGAAATGAA AACAGTCTTT TTATAGCCTT TAGCTTGTGA GTTTGGAAGT TTGGGGGGTC 60
60 TTATGTTTGT TTTCCTCTT CTGTTTCTTG GAGGAGAGTT GAGGCTTTTC TTAGGTGCAT 120

	ACACAGACCC AGGTGAACAC GCTGACTGTG AACCTGCCCT GTATCCGGAG CTGTGCTGGG	180
	CACTGAGGGG ATGCAACAAA ATTAGGAGAG GWTCCCTTGCT CCCAACGTCT ACTTCTCCTA	240
5	CCTCAACAGG GGTCCAGGGT GCAGTGAAC T CAGTTCTTGG CCCTTGGGTG AGGATTCATG	300
	GATGAATGAA AGCTAGACCT GATGGGGAGG CATTATGACT AAATAGGCCC AGCCTCCTTC	360
10	CCTTCCAGCT CTGTCCTAGG AGCATAGGCG GGAAATCTGA GTAGAGTCTG ACTGCAGTTT	420
	TTGCTTATGA TTTGTAAAAG CCGTCATGGG GTCAATAAGA AAATAGGGGT GATGGAGGGG	480
	GAGAAGCCCA GGACTGGGAG AATCGCACGT GCCCAGGGG TTTTCACCAA GGATTTTCAA	540
15	GACAAACTGG AGTAAGAATT AAAGCCCCAG AGGATTTAAT TATCCTGGTT TGCAAAAGAG	600
	CCTCCCATGC CAGTACCGCC CAGCCTTGGA GGCCGAATG CTCATGGCCC CTGTGGTCTG	660
20	CTTGTCCTTC AGCCCATGCC CAGCAGATAC CTCTCTGACT GGAGACGGGC TCAAAGCTGG	720
	ATTAGAAAGG GGAGMGGCAC TTGTGACTTT GTTTGACTCT GTGACTCACT TCCTCGCTCA	780
	CACCTTGT TT GAAC TACTGG ACTTTCAACT GGCTTTCTTT AGGTCAGGCA AGCAGACAGC	840
25	TCCCCACTGA AGAGGTCTGT ACAGTGACAA CCCGGGCCGG CAGCAAGGAC ACAGATGCAG	900
	CCACAGTAAG GCTCCATCAG GACTGGGTCA GTGATGGCAA CAGGATGGCC AAGGATGGCT	960
30	CTAGAACAYT CTGTCCATGC GTCAC TCCCC CCAGTTTTRT TTTTAGCTTT GGCTTCAGGG	1020
	AGTGACAGCC ATCACAAATA GCCACATTCT GCTCTACTCT CCAACATACC AGATTSTACA	1080
	CTGTTGTAT TT CATGAGAC GTGAATGTTG CAGAGAGTGG GGGGATCTG GTTGTTAAGG	1140
35	AACTTACACT GGGGAGCTTT ACTCTTCCGT GTCAACAATG TGACTACATG TTC TCCAGAT	1200
	TAGCCACACA TGCAACATC AGTGTCCCTC TAGCTTTANC CGAGAAAGAA ACCAGTCCCA	1260
40	GGGAATGAAT GGTGGTCTCC CCACTCCCGG CAGCACTTTA GGCAGCCCAT AAGCTATGCG	1320
	AGAATGTGAA CGCTCACCTT GCTCCGTCAC GGTCTTGACC TACCACATAA ACAGGAAGAA	1380
	GCCAGTGACC GGAACAGCTC TAGGAATAAC AAGTCAGAAT AGAAGTGTCC TTTATATTAC	1440
45	CAGAAAATAT GGGCTTG GCC TAAGTCGCTG TCTCCTAACC TGCCGGGGTC ATTCCCCACC	1500
	AAACACCCCA TACTAAGGAG CCATGAGCCA CCTGGACATT CACCTTTTCT TTGACCATCT	1560
50	GGAGTCTGGG GCAACTTAAG GAAGGCNCCA CACAGTGGTG CAGGCACATT TCCAAGCGTA	1620
	GGTGTCCCTG GCTTTTGTGG CCAAAGCTAG TGTATGGTC AACAACAGGC CAGGGTCTGT	1680
	GGGGCACTGA CCTTGAAAGT GGCAAAATGG AGGTTTCACA GGCTGTGCGG GAGCAGGACG	1740
55	GCTTGCTTCA TCTAACAATC TCAGTTTCCT TTAATAAAG AAAGAAAGGA AAAGATTTCA	1800
	TAAGCAGGTG TCAGTGGACA GTTTAAGYAC TTAACCATTT CTCTTTCTTC TTATGGATGT	1860
60	GAACTGTGCT GTGGATAAAT CATTTGTATT TCTTGAATGT TCTCTATGAC TAACAGTTAT	1920

TAAGTCGGTT GTGTATATGT GTAAC TAATG TAACTGCCTT TTAAAATTTC ATTACAATAA 1980
 AAATGACTTT GCTCTGAAMA AAAAAAAAAA AAAA ACTCGA 2020

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(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2432 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

ATGAAGGGTC GTTGGTGGGA AAGATGGCGG CGACTCTGGG ACCCCTTGGG TCGTGGCAGC 60
 20 AGTGGCGGCG ATGTTTGTCG GCTCGGGATG GGTCCAGGAT GTTACTCCTT CTTCTTTTGT 120
 TGGGGTCTGG GCAGGGGCCA CAGCAAGTCG GGGCGGGTCA AACGTTCGAG TACTTGAAAC 180
 25 GGGAGCACTC GCTGTCGAAG CCCTACCAGG GTGTGGGCAC AGGCAGTTCC TCACTGTGGA 240
 ATCTGATGGG CAATGCCATG GTGATGACCC AGTATATCCG CCTTACCCCA GATATGCAAA 300
 GTAAACAGGG TGCCTTGTGG AACCGGGTGC CATGTTTCCT GAGAGACTGG GAGTTGCAGG 360
 30 TGCACTTCAA AATCCATGGA CAAGGAAAGA AGAATCTGCA TGGGGATGGC TTGGCAATCT 420
 GGTACACAAG GAATCGGATG CAGCCAGGGC CTGTGTTTGG AAACATGGAC AAATTTGTGG 480
 35 GGCTGGGAGT ATTTGTAGAC ACCTACCCCA ATGAGGAGAA GCAGCAAGAG CGGGTATTCC 540
 CCTACATCTC AGCCATGGTG AACAACGGCT CCCTCAGCTA TGATCATGAG CGGGATGGGC 600
 GGCCTACAGA GCTGGGAGGC TGCACAGCCA TTGTCCGCAA TCTTCATTAC GACACCTTCC 660
 40 TGGTGATTCTG CTACGTCAAG AGGCATTTGA CGATAATGAT GGATATTGAT GGCAAGCATG 720
 AGTGGAGGGA CTGCATTGAA GTGCCCGGAG TCCGCCTGCC CCGCGGTAC TACTTCGGCA 780
 45 CCTCTCCAT CACTGGGGAT CTCTCAGATA ATCATGATGT CATTTCTCTG AAGTTGTTTG 840
 AACTGACAGT GGAGAGAACC CCAGAAGAGG AAAAGCTCCA TCGAGATGTG TTCTTGCCCT 900
 CAGTGACAA TATGAAGCTG CCTGAGATGA CAGCTCCACT GCCGCCCTG AGTGGCCTGG 960
 50 CCCTCTTCTT CATCGTCTTT TTCTCCCTGG TGTTTTCTGT ATTTGCCATA GTCATTGGTA 1020
 TCATACTCTA CAACAAATGG CAGGAACAGA GCCGAAAGCG CTTCTACTGA GCCCTCCTGC 1080
 55 TGCCACCACT TTTGTGACTG TCACCCATGA GGTATGGAAG GAGCAGGCAC TGGCCTGAGC 1140
 ATGCAGCCTG GAGAGTGTTC TTGTCTCTAG CAGCTGGTTG GGGACTATAT TCTGTCACTG 1200
 GAGTTTGTAA TGCAGGGACC CCGCATTTCC ATGGTTGTGC ATGGGGACAT CTAACCTCTG 1260
 60

	TCTGGGAAGC CACCCACCCC AGGGCAATGC TGCTGTGATG TGCCTTTCCC TGCAGTCCTT	1320
	CCATGTGGGA GCAGAGGTGT GAAGAGAATT TACGTGGTTG TGATGCCAAA ATCACAGAAC	1380
5	AGAATTTTCAT AGCCCAGGCT GCCGTGTGTG TTGACTCAGA AGGCCCTTCT ACTTCAGTTT	1440
	TGAATCCACA AAGAATTAAA AACTGGTAAC ACCACAGGCT TTCTGACCAT CCATTCTGTG	1500
10	GGTTTTGCAT TTGACCCAAC CCTCTGCCTA CCTGAGGAGC TTTCTTTGGA AACCAGGATG	1560
	GAAACTTCTT CCCTGCCTTA CCTTCCTTTC ACTCCATTC TGTCTCTC TGTGTGCAAC	1620
	CTGAGCTGGG AAAGGCATTT GGATGCCTCT CTGTTGGGGC CTGGGGCTGC AGAACACACC	1680
15	TGCGTTTCAC TGGCCTTCAT TAGGTGGCCC TAGGGAGATG GCTTTCTGCT TTGGATCACT	1740
	GTTCCCTAGC ATGGGTCTTG GGTCTATTGG CATGTCCATG GCCTTCCCAA TCAAGTCTCT	1800
20	TCAGGCCCTC AGTGAAGTTT GGCTAAAGGT TGGTGTAATA ATCAAGAGAA GCCTGGAAGA	1860
	CATCATGGAT GCCATGGATT AGCTGTGCAA CTGACCAGCT CCAGGTTTGA TCAAACCAAA	1920
	AGCAACATTT GTCATGTGGT CTGACCATGT GGAGATGTTT CTGGACTTGC TAGAGCCTGC	1980
25	TTAGCTGCAT GTTTTGTAGT TACGATTTTT GGAATCCAC TTTGAGTGCT GAAAGTGTA	2040
	GGAAGCTTTC TTCTTACACC TTGGGCTTGG ATATTGCCCA GAGAAGAAAT TTGGCTTTTT	2100
30	TTTTCTTAAT GGACAAGAGA CAGTTGCTGT TCTCATGTC CAAGTCTGAG AGCAACAGAC	2160
	CCTCATCATC TGTGCCCTGGA AGAGTTCATG GTCATTGAGC AGCACAGCCT GAGTGCTGGC	2220
	CTCTGTCAAC CCTTATTCCA CTGCCTTATT TGACAAGGGG TTACATGCTG CTCACCTTAC	2280
35	TGCCCTGGGA TTAAATCAGT TACAGGCCAG AGTCTCCTTG GAGGGCCTGG AACTCTGAGT	2340
	CCTCCTATGA ACCTCTGTAG CCTAAATGAA ATTCTTAAAA TCACCGATGG AACCAAAAAA	2400
40	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	2432

45 (2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

55	GACGCTGGGG GCGGGTGGGG GCGCGGGGTA CCGGGCTGGA CGGCCGGCCG GCGCCCCCTC	60
	ATTAGTATGC GGACGAAGCG GCGGGCTGCG CGGAGNGACG TCCCCTGCAG CCGCGGACCG	120
	AGGCAGCGGC GGCACCTGCC GGCCGAGCAA TGCCAAGTGA GTACACCTAT GTRAACTGA	180
60	GAAGTGATTG CTCGAGGCCT TCCCTGCAAT GGTACACCCG AGCTCAAAGC AAGATGAGAA	240

	GGCCCAGCTT GTTATTAAAA GACATCCTCA AATGTACATT GCTTGTGTTT GGAGTGTGGA	300
5	TCCTTTATAT CCTCAAGTTA AATTATACTA CTGAAGAATG TGACATGAAA AAAATGCATT	360
	ATGTGGACCC TGACCATGTA AAGAGAGCTC AGAAATATGC TCAGCAAGTC TTGCAGAAGG	420
	AATGTCGTCC CAAGTTTGCC AAGACATCAA TGGCGCTGTT ATTTGAGCAC AGGTATAGCG	480
10	TGGACTTACT CCCTTTTGTG CAGAAGGSCC CCAAAGACAG TGAAGCTGAG TCCAAGTACG	540
	ATCCTCCTTT TGGGTTCGGG AAGTTCTCCA GTAAAGTCCA GACCCCTCTG GAACTCTTGC	600
15	CAGAGCACGA CCTCCCTGAA CACTTGAAAG CCAAGACCTG TCGGCGCTGT GTGGTTATTG	660
	GAAGCGGAGG AATACTGCAC GGATTAGAAC TGGGCCACAC CCTGAACCAG TTCGATGTTG	720
	TGATAAGGTT AAACAGTGCA CCAGTTGAGG GATATTGAGA ACATGTTGGA AATAAACTA	780
20	CTATAAGGAT GACTTATCCA GAGGGCGCAC CACTGTCTGA CCTTGAATAT TATTCCAATG	840
	ACTTATTTGT TGCTGTTTTA TTTAAGAGTG TTGATTTCAA CTGGCTTCAA GCAATGGTAA	900
25	AAAAGGAAAC CCTGCCATTC TGGGTACGAC TCTTCTTTTG GAAGCAGGTG GCAGAAAAA	960
	TCCCACTGCA GCCAAAACAT TTCAGGATTT TGAATCCAGT TATCATCAA GAGACTGCCT	1020
	TTGRACATCC TTCAGTACTC AGAGCCTCAG TCAAGGTTCT GGGGGCCGAG ATAAGAACGT	1080
30	CCCCACAATC GGTGTCATTG CCGTTGTCTT AGCCACACAT CTGTGCGATG AAGTCAGTTT	1140
	GGCGGGTTTT GGATATGACC TCAATCAACC CAGAACACCT TTGCACTACT TCGACAGTCA	1200
35	ATGCATGGCT GCTATGAACT TTCAGACCAT GCATAATGTG ACAACGGAAA CCAAGTTCCT	1260
	CTTAAAGCTG GTCAAAGAGG GAGTGGTGAA AGATCTCAGT GGAGGCATTG ATCGTGAATT	1320
	TTGAACACAG AAAACCTCAG TTGAAAATGC AACTCTAACT CTGAGAGCTG TTTTGTACAG	1380
40	CCTTCTTGAT GTATTTCTCC ATCCTGCAGA TACTTTGAAG TGCAGCTCAT GTTTTAACT	1440
	TTTAATTTAA AAACACAAAA AAAATTTTAG CTCTTCCCAC TTTTPTTTTC CTATTTATTT	1500
45	GAGGTCAGTG TTTGTTTTTG CACACCATTT TGTAAATGAA ACTTAAGAAT TGAATTGGAA	1560
	AGACTTCTCA AAGAGAATTG TATGTAACGA TGTGTWTTG ATTTTAAAGA AAGTAATTTA	1620
	ATTTGTAAAA CTTCTGCTCG TTTACACTGC ACATTGAATA CAGGTAATA ATGGAAGGA	1680
50	GAGGGGAGGT CACTCTTTTG ATGGTGGCCC TGAACCTCAT TCTGGTTCCC TGCTGCGCTG	1740
	CTTGGTGTGA CCCACGGAGG ATCCACTCCC AGGATGACGT GCTCCGTAGC TCTGCTGCTG	1800
55	ATACTGGGTC TGCGATGCAG CGGCGTGAGG CCTGGGCTGG TTGGAGAAGG TCACAACCCT	1860
	TCTCTGTTGG TCTGCCTTCT GCTGAAAGAC TCGAGAACCA ACCAGGGAAG CTGTCCTGGA	1920
	GGTCCCTGGT CGGAGAGGGA CATAGAATCT GTGACCTCTG ACAACTGTGA AGCCACCCTG	1980
60	GGCTACAGAA ACCACAGTCT TCCAGCAAT TATTACAATT CTTGAATTCC TTGGGGATTT	2040

5 TTTACTGCCC TTTCAAAGCA CTTAAGTGTT AGATCTAACG TGTTCAGTG TCTGTC TGAG 2100
 GTGACTTAAA AAATCAGAAC AAAACTTCTA TTATCCAGAG TCATGGGAGA GTACACCCTT 2160
 TCCAGGAATA ATGTTTTGGG AAACACTGAA ATGAAATCTT CCCAGTATTA TAAATTGTGT 2220
 ATTTAAAAAA AAGAACTTT TCTGAATGCC TACTGGCGGT GTATACCAGG CAGTGTGCCA 2280
 10 GTTTAAAAAG ATGAAAAAGA ATAAAACTT TTGAGGAAMA AAAAAAAAAA AAAAAGTCGA 2340

15 (2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

25 AGTAGGGGAG ACTGAGACTG ACCGGTAGCC AGGCAGGCGG ACGACGCACG CCCGGACAGA 60
 CTGAGCAGGC GCCGGAGAAC CACTCACAGG TTCCCCCGCG CTTTCCCTTT GAAANCTAGG 120
 CTTTGCCTT TCCCGTGGCG CCCGAGAGAG AATGCTGGAC TCTGCCGACT TCAGCGCAAC 180
 30 TAANGATTTC TCAAGCTAGG GGACAAACGA TCAGCCCAAT CCTGAGAAGG GGGGAACCAA 240
 GCACCCCGTC CCCATCCCCC TCCCCTCCCC CGACTAAACT CGGGCGCCAA ACCCAGCCCT 300
 35 TCTCTAACCA CCCTACTTCC TCCTCTCCTT TCTAGCATGG TGGCTGTATG GACAGTCTGA 360
 CAGAACAGAG ACTGACATCT CCAATCTGC CGGCCCCCA CCTGGAACAC TACAGTGPTC 420
 TGCATTGCAC CATGACCCTG GATGTGCAA CTGTAGTCGT TTTTGCCGTG ATTGTAGTCC 480
 40 TCCTGCTTGT CAATGTCATA CTCATGTTTT TCCTGGGAAC GCGCTGAATG GAGTCCAGNC 540
 ACCTGAGCTG TCGCGAACTC TCGCTTTGAT TTCATCCCGA GAGCCACCGA GAAGAAAAAA 600
 45 A 601

50 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

60 CTCGTGCCGA ATTCGGCACG AGAGATGGTA CTTTAAAGAG GTAATTAGGT TGCTAAGATG 60

5 GATTAACATC TTCTCTTGA CACTGAGACT GGGTTCTCCT GGAATGGTT AGTTCCAAG 120
 AGAGTGAGTT GTTATAAAC AATGCTGCCT CTCTATTTT GCGTTTGTG TTTCACAAA 180
 CTCGGTCCCC TTCTGTTTCT CTACGATGTT TTGATGCRGC ATGAGGCAGT CATGAGAACC 240
 CACCAGATAC AGCTGCCTGA TCCTGAATTT CCCAGCCAAC AGAACCAAGT GCTAAATAAA 300
 10 ACTCTTTTTA ATAAGTTAAA AAAAAAAAAA AAAAAAAAAA AANAAANANA AAAAAAAAAA 359

15 (2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1141 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

25 GGCACGAGCT GCTGAGGCGT GAGAATGGCG TCCCGCGGCC GCGTCCGGA GCATGGCGGA 60
 CCCCAGAGC TGTTTATGA CGAGACAGAA GCCCGGAAAT ACGTTCGCAA CTCACGGATG 120
 30 ATTGATATCC AGACCAGGAT GGCTGGGCGA GCATTGGAGC TTCTTTATCT GCCAGAGAAT 180
 AAGCCCTGTT ACCTGCTGGA TATTGGCTGT GGCCTGGGC TGAGTGAAG TTATCTGTCA 240
 GATGAAGGCG ACTATGCGGT GGGCCTGGAT ATCAGCCCTG CCATGCTGGA TGAGGCTGTG 300
 35 GACCGAGAGA TAGAGGAGA CCTGCTGCTG GGGGATATGG GCCAGGGCAT CCCATTCAAG 360
 CCAGGCACAT TTGATGGTTG CATCAGCAT TCTGCTGTGC AGTGGCTCTG TAATGCTAAC 420
 AAGAAGTCTG AAAACCCTGC CAAGCGCCTG TACTGCTTTT TTGCTTCTCT TTTTCTGTG 480
 40 CTCGTCCGGG GATCCCGAGC TGTCTGCAG CTGTACCCTG AGAACTCAGA GCAGTTGGAG 540
 CTGATCACAA CCCAGGCCAC AAAGGCAGGC TTCTCCGGTG GCATGGTGGT AGACTACCCT 600
 45 AACAGTGCCA AAGCAAAGAA ATTCTACCTC TGCTTGT TTTT CTGGGCCTTC GACCTTTATA 660
 CCAGAGGGGC TGAGTGAAAA TCAGGATGAA GTTGAACCA GGGAGTCTGT GTTACCAAT 720
 50 GAGAGGTTCC CATTAAGGAT GTCGAGGCGG GGAATGGTGA GGAAGAGTCG GGCATGGGTG 780
 CTGGAGAAGA AGGAGCGGCA CAGGCGCCAG GGCAGGAAG TCAGACCTGA CACCCAGTAC 840
 ACCGCGCCGA AGCGCAAGCC CCGCTTCTAA GTCACCACGC GGTCTGGAA AGGCACTTGC 900
 55 CTCTGCACCT TTCTATATTG TTCAGCTGAC AAAGTAGTAT TTTAGAAAAG TTCTAAAGTT 960
 ATAAAAATGT TTTCTGCAGT AAAAAAAAAA TTCTCTGGGC CGGGCGTGGT GGCTCACACC 1020
 60 TGTAATCCCA GCACCTTGGG AGGCTGAGGT GGGAGGATCA TTTGAGGCCA GGAGTTTGAG 1080

ACCTGCCTGG GCAACATAAT GAAACTTCCT TTCCAGGGAG AAAAAAAAAA AAAAAAAAAA 1140

A 1141

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(2) INFORMATION FOR SEQ ID NO: 55:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1560 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TCCTTCTCTG GGGCGGTCGC GTTGGCAGCG GATGCGGGAA GCCGGACTCT GGGCGTCATG 60

20 TACTACAAGT TTAGTGGCTT CACGCAGAAG TTGGCAGGAG CATGGGCTTC GGAGGCCTAT 120

AGCCCGCAGA TTNAAGCCT GTGGTTTCCA CAGAAGCACC ACCTATCATA TTTGCCACAC 180

25 CAACTAAACT GACCTCCGAT TCCACAGTGT ATGATTATGC TGGGAAAAAC AAAGTTCCAG 240

AGCTACAAAA GTTTTCCAG AAAGCTGATG GTGTGCCCGT CTACCTGAAA CGAGGCCTGC 300

CTGACCAAAT GCTTTACCGG ACCACCATGG CGCTGACTGT GGGAGGGACC ATCTACTGCC 360

30 TGATCGCCCT CTACATGGCT TCGCAGCCCA AAAACAAATG AGTTAGGCTG CAGAGGACTG 420

GTTTGTTTTT TGGCATAAAC CCTTTGAAGT TCCTTTTTCA TTGTTAAATT AAAATTTTTT 480

35 TTTTACTTGT GATGGCTTAA CATTTTGTGA AGAAAAATAG GAAGATATGA AGATGATGTT 540

TTGGTTTGT TATGAAATGC ATATGGCTTG TCAGAGCTCA TTCGACAGTT AAAGCCATTG 600

TTTAAAGAAA CGGTGCTTTG CTCTGTGTTT GTGCTCCTGA TTTCCCTGGA GGTTCCTGGAT 660

40 GAAGGCTGAA CACAGGCTTG TTAATGTCAG TCTGTGCTGA GGACCTCAGG GACTTGAGGT 720

TGCATTTTTG AGCATGGGGT GCAGGAGCCT TTCTGGATTT GGATGTGGCT ATGGAAAGAA 780

45 CACAGAAAGC AAGGTCATGT GCATGAAATG AGGAGTTTGA GTTAGTCACC TCGGGGATTT 840

TTTCCATTTT GCAGTAAAT GTTAAATTAA TGTAGCCTGC CTCTATTGTG TGGGCAGGTA 900

ATTTCAAAGG GTTATTTGCC TCATCTCCTA TCTTTAGTGA AATCTTATGT GTAATGTGT 960

50 GTATTTATTC CACCGTGGGA ACAGAGAATA CCTGTTTAGT GTTGCACTTT AGACTGGTGT 1020

CTGTTTTGTT AATGCAGCTG TGCCACAAAT TCTCCTTTAT CTTTTAAAAA TGTATAGCT 1080

55 TTAAATTTTG ATTTATTTTG ACTGTGGAAT AAATACATGA ATGAAAAATT TTAAGTTTGA 1140

AGTTCTTTGA ATGACCTTTC AGAGTAATTT CAGAACACCA GCAGCATCTT AAACCTGAGT 1200

CTAATTTCTT TCTGTTAAT TAGGCACCAG ATAATCTTTA TAAAATGGTC TTAAAAGCTA 1260

60 GTAATAGGAG CTTAATGGCA ATKGATGATT ACCACAKGGT TTTTATAAAA AACCTGCCTG 1320

	CCCCWAGTG AAAGGTACCT GTAACYCACA GTYCATTTAG AACTAATTT CCTYTGCYGT	1380
	CATGATTGGK AGACTTCACT TACCCTATAT TAAITTTTGAA AAAAGGTGGA ATTTTATTAT	1440
5	ATATGAAGGA ATAGTTTGTA TCTTACCATA GCACAGAACA GTGACCTCTT GCTCAGGATA	1500
	AGATGTGGTG ATTTGAAAAT ACTCATAGTA GCCTTGCAGT GATACCTCTC TCNCTCTCTC	1560
10		
	(2) INFORMATION FOR SEQ ID NO: 56:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1507 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:	
	GGAACGCAGA GCGGAGCGTG GAGAGCGGAG CGAAGCTGGA TAACAGGGGA CCGATGATGT	60
25	GGCGACCATC AGTTCTGCTG CTCTGTGTC TACTGAGGCA CGGGGCCAG GGAAGCCAT	120
	CCCCAGACGC AGGCCCTCAT GGCCAGGGGA GGGTGCACCA GCGGGCCCC CTGAGCGACG	180
	CTCCCCATGA TGACGCCAC GGAACCTCC AGTACGACCA TGAGGCTTTC CTGGGACGGG	240
30	AAGTGGCCAA GGAATTCGAC CAACTACCC CAGAGGAAAG CCAGGCCCGT CTGGGGCGGA	300
	TCGTGGACCG CATGGACCGC GCGGGGACG GCGACGGCTG GGTGTCGCTG GCCGAGCTTC	360
35	GCGCGTGGAT CGCGCACACG CAGCAGCGGC ACATACGGGA CTCGGTGAGC GCGGCCTGGG	420
	ACACGTACGA CACGGACCGC GACGGGCGTG TGGGTGGA GGAGCTGCGC AACGCCACCT	480
	ATGGCCACTA CGCGCCCGGT GAAGAATTTC ATGACGTGGA GGATGCAGAG ACCTACAAA	540
40	AGATGCTGGC TCGGGACGAG CGGCGTTTCC GGGTGGCCGA CCAGGATGGG GACTCGATGG	600
	CCACTCGAGA GGAGCTGACA GCCTTCCTGC ACCCCGAGGA GTTCCCTCAC ATGCGGGACA	660
45	TCGTGATTGC TGAAACCCTG GAGGACCTGG ACAGAAACAA AGATGGCTAT GTCCAGGTGG	720
	AGGAGTACAT CGCGGATCTG TACTCAGCCG AGCCTGGGGA GGAGGAGCCG GCGTGGGTGC	780
	AGACGGAGAG GCAGCAGTTC CGGGACTTCC GGGATCTGAA CAAGGATGGG CACCTGGATG	840
50	GGAGTGAGGT GGGCCACTGG GTGCTGCCCC CTGCCCAGGA CCAGCCCCTG GTGGAAGCCA	900
	ACCACCTGCT GCACGARAGC GACACGGACA AGGAYGGGCG GCTGAGCAAA GCGSAAATCC	960
55	TGGGTAATTG GAACATGTTT GTGGGCAGTC AGGCCACCAA CTATGGYGAG GACCTGACCC	1020
	GGCACCACGA TGAGCTGTGA GCMCCNGCA CCTGCCACAG CCTCAGAGGC CCGCACAATG	1080
60	ACCGGAGGAG GGGCCGCTGT GGTCTGGCCC CCTCCCTGTC CAGGCCCCGC AGGAGGCAGA	1140

TGCAGTCCCA GGCATCCTCC TKCCCCTGGG CTCTCAGGGA CCCCCTGGGT CGGCTTCTGT 1200
 CCCTGTCACA CCCCCAACCC CAGGGAGGGG CTGTCATAGT CCCAGAGGAT AAGCAATACC 1260
 5 TATTCTGAC TGAGTCTCCC AGCCAGACC CAGGGACCCT NGGCCCCAAG CTCAGCTCTA 1320
 AGAACCGCCC CAACCCCTCC AGCTCCAAAT CTGAGCCTCC ACCACATAGA CTGAAACTCC 1380
 10 CCTGGCCCCA GCCCTCTCCT GCCTGGCCTG GCCTGGGACA CCTCCTCTCT GCCAGGAGGC 1440
 AATAAAAGCC AGCGCCGGGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
 AAAAAAN 1507

15

(2) INFORMATION FOR SEQ ID NO: 57:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAATTCGGCA CGAGCAGTGT CCAACACTGT AGCTGGTGCC TGCCAGGTTC CCAGTGGCTG 60
 30 GGGTCACCAG GTCTGAAGAG AGATGTGCTG GCTGCGGGCA TGGGSCCAGA TCYTCCTGCC 120
 AGTPTTCYTC TCCYTCTTTC TCATCCAATT GCTTATCAGC TTCTCAGAGA ATGGTTTTAT 180
 CCACAGCCCC AGGAACAATC AGAAACCAAG AGATGGGAAT RAAGAGGAAT GTGCTGTAAA 240
 35 GAAGAGTTGT CAATTGTGCA CAGAAGATAA GAAATATATG ATGAATAGAT AATTGAAAAG 300
 AGATCCTCCA GAAAGAGCAG AAGGAAGTTT CTCAATGGC TTCCTTCAGG ATTTTAATCA 360
 40 TCCTTACAGC CTCTTTGAGA ATGATTGAAC TTCCAAATTC CCTGAAGTTA AAATTTTAAA 420
 TTCTATTAAA CATTTTTTCG AGTAAAAAAA 450

45

(2) INFORMATION FOR SEQ ID NO: 58:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGCACGAGAC CCATTGAGCA GAAGGAGGCC AGGTGGGAAA GCTCCTGGGA AGAGCAGCCA 60
 60 GACTGGACAC TGGGCTGCTT GAGTCCTGAG TCACAATTCA GAATTCCTGG GCTCCCTGGG 120

	TGCATTTCTAT CATTCAGTT GAAAGTTTGC TTCCTTCCAG TCATGTGGCT CTTCAATCTA	180
	CTCTCCTTGG CTCTCATTTT AGATGCCATG GTCATGGATG AAAAGGTCAA GAGAAGCTTT	240
5	GTGCTGGACA CGGCTTCTGC CATCTGCAAC TACAATGCCC ACTACAAGAA TCACCCCAAA	300
	TACTGGTGCC GAGGCTATTT CCGTGACTAC TGCAACATCA TCGCCTTCTC CCCTAACAGC	360
10	ACCAATCATG TGGCCCTGAA GGACACAGGG AACCAGCTCA TTGTCACTAT GTCCTGCCTG	420
	AACAAAGAAG ACACGGGCTG GTACTGGTGT GGCATCCAGC GGGACTTTGC CAGGGATGAC	480
	ATGGATTTTA CAGAGCTGAT TGTAACAGAC GACAAAGGAA CCTGGCCAAT GACTTTGGTC	540
15	TGGGAAAGAC TATCAGGCAC AAAACCAGAA GCTGCAAGGC TCCCAAAGTT GTCCGCAAGG	600
	CTGACCGCTC CAGGACGTCC ATTCTCATCA TTTGCATACT GATCACGGGT TTGGGAATCA	660
20	TCTCTGTAAT CAGTCATTTG ACCAAAAGGA GGAGAAGTCA AAGGAATAGA AGGGTAGGCA	720
	ACACTTTGAA GCCCTTCTCG CGTGTCTGA CTCCAAAGGA AATGGCTCCT ACTGAACAGA	780
	TGTGACTGAA GATTTTTTTA ATTTAGTTCA TAAAGTGATG CTACAACAGA ATAATCACCA	840
25	TGACAACTGG CCCACACCT CAGAGACTGA TTCTGATCTC CCAGGAATTC TGAAGGTCCC	900
	TCTATCCTTG ACAACAATCA TTTGCAGCCA GGTAGCAACG GCAGTAGTCA GAGGAGCTAT	960
30	GATAGACCAC ACCCAAGCAA GGCTGCCCTC AAATAACATC TCAAGATCTT AGTTCTTATG	1020
	CATTCCATCA GTCAGAAGTG AAGAAGAGGT GGAGAATCTG GATTGGGGAC CAGGAAATCA	1080
	CTTGTATTTT GTTAGCCAAT AAATTCCTAG CCAGTGTTGA ATGAAAAAA AAAAAAAAAA	1140
35	AAAAAA	1147

40 (2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

50	GGCAGAGGCT CCTCAGAAGG GCGTGGGCTC TCCAGTCTTC CACAGTCCCC ACCATGCCCT	60
	GTTGCCTTAC CGCTGACGTA GCTCACCCAT CTTTACTTTG CCTGGCTAAG ATGCATGGCA	120
55	TYWCATTTCC TCCTTGTTGC ACTGCAGTCA GTCCCTCACT GCCCCATCT CCTGGAAGAG	180
	GAGCATAAGC TTTGCAAGGT CAGCCACTTC TCTGGGTCA CACTAGTTAC ATCAAGACAG	240
	GACTCCAGCT CATATGTGCC AGTGCAGACA CTCTTCATCC ACCTGGGGCC CTGGGCTTGG	300
60	GACCTGGYTC CTTGCACAGC AGARGACCCG GAGGCTGAGA GGAGCTTGCG GTTGTGTCAT	360

5 AGTCACCTGG CCAGARGGAA CGTGAGCCCC TCCCAAGCTG CAGARGGARG GARCARGCGT 420
 GGCTGTCAGC ACCGAGGTAG CAGAGAATTA ACATTCTTGT CAGCAGAGAA TGAAGCAGGA 480
 ATATAATTAA AACTTTGCCC TTGGAATAGC TGATTCATTT GAATTTTATT CCACACGTTT 540
 GAAAGAGGAA AGAAAATGTG AAGACTTGCA GCCTGGTTCT CGCCTGGCCT GGGCTGGCCC 600
 10 AGCTGTCAGG CCCGGTTCCT TTCTGAGCAT TCAGTCCACT GATGTTGACT GAGGGCCAGG 660
 AGAGACCCTC AGCAGGGTAT TACCATATCA GCCTCCTATC GCTGCTGGGA GAAATTACCA 720
 15 TGAATTCAGT GGCTTAAAAC AACACACGAG CCTCTCTGAG CCTACCCTGG CTCAGGA 777

20 (2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

30 AAGANTGATT TTCCTTACTC TCCAAAGCGT CAGCATTTTG AAGTTTCTTT TATGAAAGTG 60
 GGGGCAAGAA TCAGGGTGAA AATGAGTGTA AACAAAGCCC ATCCTGTGGT CAGCACCCAC 120
 TGGAGGTGGC CAGCAGAGTG GCTTCAGATG TTCCTGCACC TGGCCCAGGA GCCCAGGACA 180
 35 GAGGTCAAAT CTAGGCCCTT TGGTCTGGCT GGATTCATCA GGCAAGATTC GAAAACAAGA 240
 AAACCTCTAG AACAAGAAAC AATCATGTCT GCAGCAGATA CGGCACTGTG GCCCTATGGC 300
 40 CATGGCAATC GTGAGCACCA AGAGAATGAG TTACAGAAAT ATCTCCAATA CAAAGACATG 360
 CATCTCCTGG ACAGTGAGCA GTCGCTGGGA CACACACACA CACTTCAAGG CTCACACAAC 420
 CTAACAGCCT TAAATATCTG AAGAAACAGA ATCACGACAT TAAGTCAGCA GAGGGAGAGG 480
 45 TAGGCTGAAG CAGCAGGAGG CCAATTTTAT ATCCCACAGA TTTTPTTAAA AATGACTCCC 540
 CAGCAAGGGG TGGGGAGAAA GCCACTGATT TAGGAGAGTT CTTGGCTCAG CCAACCACTG 600
 CGGTTATCTA CACGTTTAC AAAGGCACRG AAGTAGAGAG GGGCTGCACT CACGACCCCTC 660
 50 CCCAGGGCCC GCACAGCCAG ACACGGTGGG TTCTTCTCTT TTCCCTTCTG GCCTTGGTGG 720
 AATTCCCTACC ACGGTGGCCT CTGCCTTTGG GACAATGCCT TCATGCTCAT CCCCAGGTCA 780
 55 AGGATGGAGT CTGTTACCAT TTTCCAGGGG AAATTCCAAG GACCAGCCCC GCCTCATTAC 840
 GTTCACCCCA CAGGAAGGTG ATCTGGAAAG CCTGTAAACA CGTACTCTGG GTGGCTGAGT 900
 60 GGTGTCACCA AGCTGCTTTT GTGCAGGGCT GAAGCACAGA CAAGAGGGCA GGCAGCTGCC 960

GGAGGCCTGA AGTGGGGAGA GATCCCCGCA GGCCTGCAGG AGCCAGGGAG AACCTCCAAC 1020
 TGGATCTAAA CTGTGGGACA GCCCAGGCGT GCCCTCTTC ACATGGCTCC CAGGCTCCCT 1080
 5 CAAAGCCCTT CCCAGGCCCT GCAGGAAGAG AGGGAGGGTG AGGAGAGGCA GGGAGGGCAG 1140
 AGGTCGCCTG AAAGCCTGGG CTCCGAACTC CCTCAGCAGA GCTTTAAAGT G 1191

10

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 1580 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCCCGCCCC CGCCACGAA GGAAGTGGCT GCTGCTCCGG CGCGGACCCA GAGCCGGTTC 60
 GGCGCGTCGA CTGCCCAGAG TCCGCGGCCG GGCGCGGGAG GAGCCAAGCC GCCATGGCCT 120
 25 ACCACAGCTT CCTGGTGGAG CCCATCAGCT GCCACGCCTG GAACAAGGAC CGCACCAGCA 180
 TTGCCATCTG CCCCACAAC CATGAGGTGC ATATCTATGA AAAGAGCGGT GCCAAATGGA 240
 30 CCAAGGTGCA CGAGCTCAAG GAGCACAACG GGCAGGTGAC AGGCATCGAC TGGGCCCCCG 300
 AGAGTAACCG TATTGTGACC TGCGGCACAG ACCGCAACGC CTACGTGTGG ACGCTGAAGG 360
 GCCGCACATG GAAGCCCACG CTGGTCATCC TCGGATCAA CCGGGCTGCC CGCTGCGTGC 420
 35 GCTGGGCCCC CAACGAGAAC AAGTTTGCTG TGGGCAGCGG CTCTCGTGTG ATCTCCATCT 480
 GTTATTTTGA GCAGGAGAAT GACTGGTGGG TTTGCAAGCA CATCAAGAAG CCCATCCGCT 540
 40 CCACCGTCCT CAGCCTGGAC TGGCACCACA ACAATGTGCT GCTGGCTGCC GGCTCCTGTG 600
 ACTTCAAGTG TCGGATCTTT TCAGCCTACA TCAAGGAGGT GGAGGAACGG CCGGCACCCA 660
 CCCCCTGGGG CTCCAAGATG CCCTTTGGGG AACTGATGTT CGAATCCAGC AGTAGCTGCG 720
 45 GCTGGGTACA TGGCGTCTGT TTCTCAGCCA GCGGGAGCCG CGTGGCCTGG GTAAGCCACG 780
 ACAGCACCGT CTGCCTGGCT GATGCCGACA AGAAGATGGC CGTCGCGACT CTGGCCTCTG 840
 50 AAACACTACC ACTGCTGGCG CTGACCTTCA TCACAGACAA CAGCCTGGTG GCAGCGGGCC 900
 ACGACTGCTT CCCGGTGTG TTCACCTATG ACGCCGCCGC GGGGATGCTG AGCTTCGGCG 960
 GGCGGCTGGA CGTTCCTAAG CAGAGCTCGC AGCGTGGCTT GACGGCCCCG GAGCGCTTCC 1020
 55 AGAACCTGGA CAAGAAGGCG AGCTCCGAGG GTGGCACGGC TCGGGGCGCG GGCCTAGACT 1080
 CGCTGCACAA GAACAGCGTC AGCCAGATCT CGGTGCTCAG CGGCGGCAAG GCCAAGTGCT 1140
 60 CGCAGTTCTG CACCACTGGC ATGGATGGCG GCATGAGTAT CTGGGATGTG AAGAGCTTGG 1200

5 AGTCAGCCTT GAAGGACCTC AAGATCAAAT GACCTGTGAG GAATATGTTG CCTTCATCCT 1260
 AGCTGCTGGG GAAGCGGGGA GAGGGGTCAG GGAGGCTAAT GGT'TGCTTTG CTGAATGTTT 1320
 CTGGGGTACC AATACGAGTT CCCATAGGGG CTGCTCCCTC AAAAAGGGAG GGGACAGATG 1380
 GGGAGCTTTT CTTACCTATT CAAGGAATAC GTGCCTTTTT CTTAAATGCT TTCATTTATT 1440
 10 GAAAAAATAA AAAAATGCCC CCAAAGCACT ATGCTGGTCA TGAAGTCTT CAAAATGTGG 1500
 AGGTAATAAA ATGCAACTGT GTAAAAAATAA AAAAAAATAA AAATGACCCT CGCGATCTAG 1560
 AACTAGNCGG ACGCNTGGGT 1580
 15

(2) INFORMATION FOR SEQ ID NO: 62:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1117 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

30 GGCACGAGGC GCGATGCAGC ACAGGCTAGA GGCTGCGCAA SGCGGGGGCC CGCCCCTGGG 60
 ACCCTCCGGG COGGGCGGTT TGGCCCTTTA GCGCCCGGGC GTCGGGGCGG TAAAAGGCCG 120
 GCAGAAGGGA GGCAC'TT'GAG AAATGTCTTT CCTCCAGGAC CCAAGTTTCT TCACCATGGG 180
 35 GATGTGGTCC ATTGGTGCAG GAGCCCTGGG GGCTGTGCCC TTGGCATTGC TGCTTGCCAA 240
 CACAGACGTG TTTCTGTCCA AGCCCCAGAA AGCGGCCCTG GAGTACCTGG AGGATATAGA 300
 CCTGAAAACA CTGGAGAAGG AACCAAGGAC TTTCAAAGCA AAGGAGCTAT GGGAAAAA 360
 40 TGGAGCTGTG ATTATGGCCG TCGGAGGCC AGGCTGTTTC CTCTGTGAG AGGAAGCTGC 420
 GGATCTGTCC TCCCTGAAAA GCATGTTGGA CCAGCTGGGC GTCCCCCTCT ATGCAGTGGT 480
 45 AAAGGAGCAC ATCAGGACTG AAGTGAAGGA TTTCCAGCCT TATTTCAAAG GAGAAATCTT 540
 CCTGGATGAA AAGAAAAAGT TCTATGGTCC ACAAAGGCGG AAGATGATGT TTATGGGATT 600
 TATCCGTCTG GGAGTGTGGT ACAACTTCTT CCGAGCCTGG AACGGAGGCT TCTCTGAAA 660
 50 CCTGGAAGGA GAAGGCTTCA TCCTTGGGGG AGTTTTCGTG GTGGGATCAG GAAAGCAGGG 720
 CATCTTCTT GAGCACCGAG AAAAGAATT TGGAGACAAA GTAAACCTAC TTTCTGTTCT 780
 55 GGAAGCTGCT AAGATGATCA AACCACAGAC TTTGGCCTCA GAGAAAAAAT GATTGTGTGA 840
 AACTGCCCAG CTCAGGGATA ACCAGGGACA TTCACCTGTG TTCATGGGAT GTATTGTTTC 900
 CACTCGTGTC CCTAAGGAGT GAGAAACCCA TTTATACTCT ACTCTCAGTA TGGATTATTA 960
 60

ATGTATTTTA ATATTCTGTT TAGGCCCACT AAGGCAAAAT AGCCCCAAAA CAAGACTGAC 1020
 AAAAATCTGA AAAACTAATG AGGATTATTA AGCTAAAACC TGGGAAATAG GAGGCTTWAA 1080
 5 ATGACTGCCM GCTGGTGCRT GCTCACACTT GGCCAC 1117

10 (2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

20 CCCACGCGTG CKGGCGCCTG GCAGCCACCG CCTGGGAGGT TACTGTAAGG CCCGCAGCTC 60
 CCGCCAGCTC CCGCGGACTS CTGCCGCCTC CTTACCATGA AGCCAGTAAG TCGTCGCACG 120
 CTGGACTGGA TTTATTCACT GTTGCTGCTT GCCATCGTTT TAATCTCCTG GGGCTGCATC 180
 25 ATCTATGCTT CGATGGTGTC TGCAAGACGA CAGCTAAGGA AGAAATACCC AGACAAAATC 240
 TTTGGGACGA ATGAAAATTT GTAACCTTTC TGGATTTAAT TATCTGAAAA TACAGTTCTT 300
 30 TCCCTCATGC TTATGTAGAT ATAAAAATAA AATTCATAAT GCAAAAAAAA AAAAAAAAAA 360
 G 361

35

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1668 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGCACGAGGT CTGCCAAGCT ATAGACCATG GCTGTGAACA CATTTGTGTG AACAGTGACG 60
 ACTCATACAC GTGCGAGTGC TTGGAGGGAT TCCGGCTCGC TGAGGATGGG AAACGCTGCC 120
 50 GAAGAAGGAT GTCTGCAAAT CAACCCACCA TGGCTGCGAA CACATTTGTG TTAATAATGG 180
 GAATTCCTAC ATCTGCAAAT GCTCAKAGGG ATTTGTTCTA GCTGAGGACG GAAGACGGTG 240
 55 CAAGAAATGC ACTGAAGGCC CAATTGACCT GGTCTTTGTG ATCGATGGAT CCAAGAGTCT 300
 TGGAGAAGAG AATTTTGAGG TCGTGAAGCA GTTTGTCACT GGAATTATAG ATTCTTGC 360
 AATTTCCCCC AAAGCCGCTC GAGTGGGGCT GCTCCAGTAT TCCACACAGG TCCACACAGA 420
 60

	GTTCACCTCTG AGAAACTTCA ACTCAGCCAA AGACATGAAA AAAGCCGTGG CCCACATGAA	480
	ATACATGGGA AAGGGCTCTA TGA CTGGGCT GGCCCTGAAA CACATGTTTG AGAGAAGTTT	540
5	TACCCAAGGA GAAGGGGCCA GGCCCTTTCC ACAAGGGTGC CCAGAGCAGC CATTGTGTTC	600
	ACCGACGGAC GGGCTCAGGA TGACGTCTCC GAGTGGGCCA GTAAAGCCAA GGCCAATGGT	660
10	ATCACTATGT ATGCTGTTGG GGTAGGAAAA GCCATTGAGG AGGAACTACA AGAGATTGCC	720
	TCTGAGCCCA CAAACAAGCA TCTCTTCTAT GCCGAAGACT TCAGCACAAAT GGATGAGATA	780
	AGTGAAAAAC TCAAGAAAGG CATCTGTGAA GCTCTAGAAG ACTCCGATGG AAGACAGGAC	840
15	TCTCCAGCAG GGGAACTGCC AAAAACGGTC CAACAGCCAA CAGTGCAACA CAGATATCTG	900
	TTTGAAGAAG ACAATCTTTT ACGGTCTACA CAAAAGCTTT CCCATTCAAC AAAACCTTCA	960
20	GGAAGCCCTT TGAAGAAAA ACACGATCAA TGCAAATGTG AAAACCTTAT AATGTTCCAG	1020
	AACCTTGCAA ACGAAGAAGT AAGAAAATTA ACACAGCGCT TAGAAGAAAT GACACAGAGA	1080
	ATGGAAGCCC TGGAAAATCG CCTGAGATAC AGATGAAGAT TAGAAATCGC GACACATTTG	1140
25	TAGTCATTGT ATCACGGATT ACAATGAACG CAGTGAGAG CCCCAAAGCT CAGGCTATTG	1200
	TTAAATCAAT AATGTTGTGA AGTAAAAA TCAGTACTGA GAAACCTGGT TTGCCACAGA	1260
30	ACAAAGACAA GAAGTATACA CTAAC TTGTA TAAATTTATC TAGGAAAAAA ATCCTTCAGA	1320
	ATTCTAAGAT GAATTTACCA GGTGAGAATG AATAAGCTAT GCAAGGTATT TTGTAATATA	1380
	CTGTGGACAC AACTTGCTTC TGCCTCATCC TGCCTTAGTG TGCAATCTCA TTTGACTATA	1440
35	CGATAAAGTT TGCACAGTCT TACTTCTGTA GAACACTGGC CATAGGAAAT GCTGTTTTTT	1500
	TGTAYTGAC TTTACCTTGA TATATGTATA TGGATGTATG CATAAAATCA TAGGACATAT	1560
40	GTACTTGTGG AACAAGTTGG ATTTTATTATA CAATATTAAA ATTCACTACT TCAGAGRAAA	1620
	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAANAAAA	1668

45

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

55

GGGTCGACCC ACGCGTCCGC CCACGCGTCC GGATGGCTGC GCTGTTGCTG AGACACGTTG 60

GTCGTCATTG CCTCCGAGCC CACTTTAGCC CTCAGCTCTG TATCAGAAAT GCTGTTCTTT 120

60

TGGAACCCAC GGCCAAAGAA GAGATGGAGC GGTCTCTGGAA TAAGAATATA GGTTCAAACC 180

5 GTCCTCTGTC TCCCCACATT ACTATCTACA GTTGGTCTCT TCCCATGGCG ATGTCCATCT 240
 GCCACCGTGG CACTGGTATT GCTTTGAGTG CAGGGGTCTC TCTTTTGGC ATGTCCGCCC 300
 TGTACTCCC TGGGAACTTT GAGTCTTATT TGGAACTTGT GAAGTCCCTG TGTCTGGGGC 360
 CAGCACTGAT CCACACAGCT AAGTTTGCAC TTGTCTTCCC TCTCATGTAT CATACTGGA 420
 10 ATGGGATCCG ACACTTGATG TGGGACCTAG GAAAAGGCCT GAAGATTCCC CAGCTATACC 480
 AGTCTGGAGT GGTGTCTCTG GTTCTTACTG TGTGTCTCTC TATGGGGCTG GCAGCCATGT 540
 GAAGAAAGGA GGCTCCAGC ATCATCTTCC TACACATTAT TACATTCACC CATCTTCTG 600
 15 TTTGTCAATC TTATCTCCAG CCTGGGAAAA GTTCTCCTTA TTTGTTTAGA TCCTTTTGTA 660
 TTTTCAGATC TCTTGGAGC AGTAGAGTAC CTGGTAGACC ATAATAGTGG AAAAGGGTCT 720
 20 AGTTTCCCC TTGTTCTAA AGATGAGGTG GCTGCAAAAA CTCCCCTTTT TTGCCCACAG 780
 CTGCGCTACT CTCGGCTAG AAGCAGTTAT TCTCTCTCCA TATTGGGCTT TGATTGTGC 840
 TGAGGGTCAG CTTTGGCTC CTTCTTCTG AGACAGTGA AACAATGCCA GCTCTGTGGC 900
 25 TTCTGCCCTG GGGATGGCC GGGTTGGGG GTGGGTGGT GAGGCTTTGG GTGCCACTGC 960
 CTGTGGGTTG CTGGCTTAA GGACAATTCT CTTCATTGGT GAGAGCCCAG GCCATTAA 1020
 30 CCTACACAGT GTTATTGAAA GAAGAGAGGT GGGGGTGGAG GGAATTAGT CTGTCCCAGC 1080
 TAGAGGGAGA TAAAGAGGC TAGTTAGTTC TTGGAGCAGC TGCTTTTGGAG GAGAAAATAT 1140
 ATAGCTTTGG ACACGAGGAA GATCTAGAAA ATTATCATG AACATATTAA TGGTTATTTC 1200
 35 TTTTCTTGG ATTTCCAGAA AAGCCTCTTA ATTTTATGCT TTCTCATCGA AGTAATGTAC 1260
 CCTTTTTTTC TGAAACTGAA TTAAATACTC ATTTTATCTT TGAAAAAAA AAAAAAACC 1320
 40 TNGGGGGGGG CCCCAGACC NAATTGGCCC TAT 1353

45 (2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

55 CGGAAGAAAG CAGCCATCCA GACATTTTCTG AACACGTACC AGGTGTTAGC TGTGACCTTC 60
 AATGACACAA GTGATCAGAT TATTTCTGGT GGAATAGACA ATGATATCAA GGTCTGGGAC 120
 60 TGCGCCAGAA CAAGCTAACC TACACCATGA GAGGCCATGC AGATTCTAGT ACTGGCCTGA 180

	GTTTAAGTTC TGAAGGCTCT TATCTTTTGT CCAATGCAAT GGACAATACA GTTCGTGTCT	240
	GGGATGTCCG GCCATTTGCC CCCAAAGAGA GATGTGTAAA GATATTTCAA GGAAATGTGC	300
5	ACAACCTTGA AAAGAACCTT CTGAGATGTT CTTGGTCACC TGATGGAAGC AAAATAGCAG	360
	CTGGCTCAGC CGACAGGTTT GTTTATGTGT GGGATACCAC AAGCAGGAGA ATATTGTATA	420
10	AGCTGCCCCG CCATGCTGGC TCCATCAATG AAGTGGCTTT CCACCCTGAT GAGCCCATCA	480
	TTATCTCAGC ATCGAGTGAC AAGAGACTGT ATATGGGAGA GATTCAGTGA AGATATGGAC	540
	TGGAAGACTC CAAGGCCGCT TGTCTTTGAG ACCTCAGACT GCATAAGTGA TGCCAAATGT	600
15	TGGATGTCCA GGYTAGCACC CTCCCTTCAG ATGACCATTG CTAGCAAGAA ACAGGAGGCG	660
	GTGGCCATAT TCCAAAAACC ACTTCTGTCC CATTTACCA GGATGACTAA GGCAAGCTCC	720
20	CTGTGGCCTC TAAAAACCAC CTGCCAGATT TCAGGGACTG TTTTTTTTTT TCTTTTTCTT	780
	TTTTCTGT TTTCTAATGCA GGCCCAATGT GACAAATTTG TTGGTTGGGA TTTTTTTTTT	840
	TTTTTGTAAC TGGCTTGAT GATATTTCT TCTGTATTT CTCTATATCA TTTGTATTA	900
25	AAAGCCAAAT AGATGCCTTT TTACAAGARM AAAAAAAAAA AAAAAAAAAA NNAAAAAAAA	960
	CTGGGAGGGG GGGCCCGGTA CCCAAATCGC CGGATATGAT CGTAAACAAT C	1011

30

(2) INFORMATION FOR SEQ ID NO: 67:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

	GGCCGGGCGG TCGCACTGC GGGCGCATCC CTGCCCCGC GCCGTCCGTG CCCGCGGGAC	60
	CTGACAGCCG GGTGAGAGG CGAACTGTGC TCAGGCCCG GCTGGACGCA GAGCCAGAGC	120
45	TGTCCCCAGA GGAGCAGAGG GTCCTGGAAA GGAAGCTGAA AAAGGAACGG AAGAAAGAGG	180
	AGAGGCAGCG TCTGCGGGAG GCAGGCCTTG TGGCCCAGCA CCCGCCTGCC AGGCGCTCGG	240
50	GGGCCGAAC TGCCTGGGAC TACCTCTGCA GATGGGCCCA AAAGCACAAG AACTGGAGGT	300
	TTCAGAAGAC GAGGCAGACG TGGCTCCTGC TGCACATGTA TGACAGTGAC AAGGTTCCTG	360
55	ATGAGCACTT CTCCACCCTG CTGGCTACC TGGAGGGGCT GCAGGGCCGG GCCCGAGAGC	420
	TGACGGTGCA GAAGGCGGAA GCCTGATGCG GGAGCTGGAT GAGGAGGGCT CTGATCCCCC	480
	CCTGCCGGGG AGGGCCAGC GCATCCGACA GNTGCTGCAG CTGCTCTCCT AGTGGGTTCA	540
60	GCGCGGGGCG GGGCCGCTGC CCAGTGCAGG GCTGCCCTCAG ACCACACAGG GTGCAGCTCC	600

5 TCCGGCGGTG GGGGCCGGGT TCACCAGCAG GGCAGCGGCT GAGCAAGGGC TTTCAGCTCC 660
 TCCGGTGGTG GGGGCCGGGA TCACCAGCAC CAGAGCCTCG CAAGGGCCCC TTCCCTCCTC 720
 CAGACCCTCC TTGGCCGGTG ACGCTGTGAC AGTGATGGCA GGTTCAGTGC CTTCAGCGCA 780
 GAGCGTGGAT GCTCTGGAAT CACCCGGACC CCTGGCCTTG GAGGGACCCT CCAGCCCCAG 840
 10 GAATCTGCTT TGGAGGGAAA TGTCTATTTT TCTACCGGA ATATTTTAGA GATTGGGGCA 900
 TGCTGGCTCC TCCC GCCAGC TGCAAACCTG CACCTTCCGC CTGATTCCCG ATCCCCCTGC 960
 GTGGGCCGCA TTCCTGGTCC CCTGCCTGCG TCCATCGAGG GGCCTGGCTG TGGCCTGTTT 1020
 15 TCCTTTGACC CCACACAGCG TCATTGCGGG TCATGGGGAG CCCCTGGTGG GAGCTTGTGG 1080
 AGTCGGATCA CGTACCTGTG CAGAAACCGC CTCTGTGGCT GCATTTGAAA TAAAACCCGA 1140
 20 CCCAGCAGCA AAAAAAAAAA AAAAAANCNC NAGGGGGGGC CCGGNACCCA ATT 1193

25 (2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

35 GAATTCGGCA CGAGTTGGCA CATGATGCAA AATGCATTC TCAGAGTAGA TTGCAGTCAA 60
 AAATGTTGGA AACTACTAAG CATGTGCARA TAGCATGCAT GCTGCTGCTG ACCTGCCAGA 120
 TATTTCTCCC TTCTCCCTT TCTCCCTCAT TTATTCAITC ATTAAGTGAT TCATTCATCC 180
 40 CATTAAGAAA ATTATATGTA TGTTTTGTGC AAAGCACCTT ACTCAAGGCT GCGGGGTACA 240
 AAAGTATATC AGAAGCCTTG GGCCTTGACM WACTTCTCTG TAGTAGTGCT AGATTTGTGT 300
 45 GGATCTGCCA CACTTACTCC AGGCCTCTTG TGACCTGTGC TTTGCATTAA TCTCTTAGGC 360
 TAAGCCACAT ACCTTTTCAT TATACAATCT TTGCTGATGC TAAGGACAGA TTCAAAGTG 420
 CCCTCCTTAT AATTTTTGTA TTTAATGCAA AGTGTAATCA AGAATAGGCC ATTGTTAGGT 480
 50 CAATTCGCTT TCTGTATTTA TCTTTTCAAA CAATAAATAA TCAGTGGGAT GAAAAAGGCC 540
 CGGAAAAAAA AAAAAAAAAA 560

55

(2) INFORMATION FOR SEQ ID NO: 69:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

	CGGACNGAGC CGCCGCCGGG CACTTCCTGT GGAGGCCGCA GCGGGTGCGG GCGCCGACGG	60
10	GCGAGAGCCA GCGAGCGAGC GAGCGAGCCG AGCCGAGCCT CCCGCCGTCG CCATGGGCCA	120
	GAACGACCTG ATGGGCACGG CCGAGGACTT CGCCGACCAG TTCCTCCGTG TCACAAAGCA	180
	GTACCTGCCC CACGTGGCGC GCCTCTGTCT GATCAGCACC TTCCTGGAGG ACGGCATCCG	240
15	TATGTGGTTC CAGTGGAGCG AGCAGCGCGA CTACATCGAC ACCACCTGGA ACTGCGGCTA	300
	CCTGCTGGCC TCGTCCCTCG TCTTCCTCAA CTTGCTGGGA CANTGACTGG CTGCGTCCTG	360
20	GTGTTGAGCA GGAACCTCGT GCAGTACGCC TGCTTCGGGC TCTTTGGAAT CATAGCTCTG	420
	CAGACGATTG CCTACAGCAT TTTATGGGAC TTGAAGTTTT TGATGAGGAA CCTGGCCCTG	480
	GGAGGAGGCC TGTGTCTGCT CCTAGCAGAA TCCCGTCTG AAGGGAAGAG CATGTTTGCG	540
25	GGCGTCCCA CCATGCGTGA GAGCTCCCC AAACAGTACA TGCAGCTCGG AGGCAGGGTC	600
	TTGTGTTTC TGATGTTTCAT GACCTCCTT CACTTTGACG CCAGCTTCTT TTCTATTGTC	660
30	CAGAACATCG TGGGGCACAG CTCTGATGAT TTTAGTGGCC APTGGTTTTA AAACCAAGCT	720
	GGCTGCTTTG ACTCTTGTTG TGTGGCTCTT TGCCATCAAC GTATATTTCA ACGCCTTCTG	780
	GACCATTCCA GTCTACAAGC CCATGCATGA CTTCTGAAA TACGACTTCT TCCAGACCAT	840
35	GTGCGTGATT GGGGGCTTGC TCCTGGTGGT GGCCCTGGGC CCTGGGGGTG TCTCCATGGA	900
	TGAGAAGAAG AAGGAGTGGT AACAGTCACA GATCCCTACC TGCCTGGCTA AGACCCGTGG	960
40	CCGTCAAGGA CTGGTTCGGG GTGGATTCAA CAAAACGACC AGCTTTTATG TATCCTCTTC	1020
	CCTTCCCCTC CCTTGGTAAA GGCACAGATG TTTTGAGAAC TTTATTGCA GAGACACCTG	1080
	AGAATCAATG GCTTCAGGAC ATGGGTCTCT TCTCCTGTG ATCATTCAG TGCTCACTGC	1140
45	ATGAAGACTG GCTGTCTCA GTGTTTCAAC CTCACCAGG CTGTCTCTTG GTCCACACCT	1200
	CGCTCCCTGT TAGTGCCGTA TGACAGCCCC CATCAAATGA CCTTGGCCAA GTCACGGTTT	1260
50	CTCTGTGGTC AAGGTTGGTT GGCTGATGG TGGAAAGTAG GGTGGACCAA AGGAGGCCAC	1320
	GTGAGCAGTC AGCACCAGTT CTGCACCAGC AGCGCCTCCG TCCTAGTGGG TGTTCCTGTT	1380
	TCTCCTGGCC CTGGGTGGGC TAGGGCCTGA TTCGGGAAGA TGCCTTTGCA GGGAGGGGAG	1440
55	GATAAGTGGG ATCTACCAAT TGATTCTGGC AAAACAATTT CTAAGATTTT TTTGCTTTAT	1500
	GTGGGAAACA GATCTAAATC TCATTTTATG CTGTATTTTA TATCTTAGTT GTGTTTGAAA	1560
60	ACGTTTGTGAT TTTTGGAAC ACATCAAAAT AAATAATGGC GTTGTGTGTA AAAAAAAAAA	1620

AAAAAACTC GRGGGGGGC CCGGTACCCA AATCGCC

1657

5

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
- 10 (A) LENGTH: 711 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

GGCACGAGCG AAGACCCTGT TCGGACCCTG CCCCATTCC AGACTCAGGT AGATCGTCGG 60
CATACCCTCT ACCGTGGACA CCAGGCAGCC CTGGGGCTGA TGGAGAGAGA TCAGGTATCC 120
20 CCCAGGGAGT AGGGGCTACC TTGAGGGGAT GATAGACCTC CCCACTCCC AGTGKKACTC 180
TGGAAATATG AAGGAACTAG GGAGTGAAG AGATTTTCTG GCTGGGGAGA GGAGTTCCTC 240
25 CCTTCAAAGC CAGCAACTGC CTTTGGGGAA TGTCTGGGGG TCTCTCCTTT CTCCTGCTTG 300
TTTRAGGTGG TACACAGTCC CCCCTTCAMC TGGSGGGAAG CTGTNCCGGA CARACTCATC 360
TCAGCTTTCC CTTGGGGCAG GATCGGGGGC AGCAGCTCCA GCAGAAACAG CAGGATCTGG 420
30 AGCAGGAAGG CCTCGAGGCC ACACAGGGGC TGCTGGCCGG CGAGTGGGCC CCACCCCTCT 480
GGRAGCTGGG CAGCCTCTTC CAGGCCTTCG TGAAGAGGGA GAGCCAGGCT TATGCGTAAG 540
35 CTTTCATAGCT TCTGCTGGCC TGGGGTGGAC CCAGGACCCC TGGGGCCTGG GTGCCCTGAG 600
TGGTGGTAAA GTGGAGCAAT CCCTTCACGC TCCTTGGCCA TGTTCCTGAGC GGCCAGCTTG 660
GCCTTTGCCT TAATAAATGT GCTTTATTTT CAAAAAAAAA AAAAAAAAAAC T 711
40

45 (2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 935 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

GGCACAGGGT GAAAGCCAGC TAAACCCCAA GTGGAGAAGT GAAAGACATG GTTGTTCCTCA 60
55 TAAGTTTATT GCTCACATTA TGAAAGAAGC CATAGTCATG AGTGAACCAC TCCCTAGGTT 120
GATAAGGAAA CCAACACGGA AGATCTCTTT CTGGAAGAAG CAGCCAGCCT CGTGAAGGAG 180
60 CGGCCAGCC GCCGGGCCCC AGGGTCGCCT TTTGTTCGGA GTGGCACGAT TGTCCGTTCC 240

CAGACATTCT CGCCTGGAGC ACGAAGCCAG TATGTTTGCA GACTTTATCG TAGTGACAGC 300
 GACAGTTCAA CGCTGCCCCG GAAGTCCCCC TTTGTCCGAA ATACTTTGGA AAGACGAACC 360
 5 CTTCGCTATA AGCAGTCATG CAGGTCTTCC CTGGCTGAGC TCATGGCCCC CACCTCCCTG 420
 GACTTGGAGC TGGATCTCCA GGCCTCGAGA ACACGGCAGA GGCAGCTGAA TGAGGAGCTC 480
 10 TCGCCCTCC GTGAGCTGCG GCAGCGGTTN GGAGGACGCC CAGCTCCGTG GCCAGACTGA 540
 CCTCCACCC TGGGTGCTTC GGGACGAGCG GCTCCGTGGC CTGCTGCGGG AGCCGAGCGG 600
 CAGACAAGAC AGACCAAAC TACTACCGT CATGAGCAGG CGGCTGAGAA GATGCTGAAG 660
 15 AAGGCCTCCA AGGAGATCTA CCAGCTGCGT GGCAGAGCCA CAAAGAGCCC ATCCAAGTGC 720
 AGACCTTTAG GGAGAAGATA GCATTCTTCA CAAGGCCAAG GATCAACATA CCTCCTCTCC 780
 20 CAGCCGACGA CGTCTGATGG AGTGCATTGT GCACATGAAG TATTTATCCA CCTGTTTTAT 840
 TTTCATGAAG TTCTTAGACT AGCTGAATTT GTCTTTAAAA TATTTGTGCA AAGCTATTAA 900
 TATACACATT TTGTAAGAAA AAAAAAAAAA AACT 935
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(2) INFORMATION FOR SEQ ID NO: 72:
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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 504 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GCAGGGGCGA GGGGYTGGGG ACCGCGGGGC GGACGGGAGC GAGTATGTCC GCTCTGACTC 60
 40 GGCTGGCGTC TTTCGCTCGC GTTGAGGCC GCCTTTTCAG AAGCGGCTGC GCACGGACTG 120
 CTGGAGATGG TGGAGTCCGT CATGCCGTG GTGGTGTGCA CATTGAGCCC CGGTATAGAC 180
 45 AGTTCCCCCA GCTGACCAGA TCCCAGGTGT TCCAGAGCGA GTTCTTCAGC GGACTCATGT 240
 GGTTCCTGGAT TCTCTGGCGC TTTTGGCATG ACTCAGAAGA GGTGCTGGGT CACTTTCCGT 300
 ATCCTGATCC TCCCAGTGG ACAGATGAAG AATTAGGTAT CCCTCCTGAT GATGAAGACT 360
 50 GAAGGTGTAG ACTCAGCCTC ACTCTGTACA AGAGCCAGGT GAGAATTTC AAGATTATCG 420
 ACTTCATATT GCACATTAAA GTTACAAATT AAAGTGGCTT GGTCAAGAAT GARAAAAAAA 480
 55 AAAAAAATT GGGGGGGGGC CCCN 504

60 (2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

10 GAATTCGGCA CGAGGAGGAG GGGAGGCGGG GTAAGTTTGG TGGGAAACTC TGTAATTTCC 60
WTTTTTACTT TCACAGCAAT AGTGCAGAAT CCAGAATGGA TGTCTCTTT GTAGCCATCT 120
TTGCTGTGCC ACTTATCCTG GGACAAGAAT ATGAGGATGA AGAAAGACTG GGAGAGGATG 180
15 AATATTATCA GGTGGTCTAT TATTATACAG TCACCCCCAG TTATGATGAC TTTAGTGCAG 240
ATTTACCAT TGATTACTCC ATATTTGAGT CAGAGGACAG GCTGAACAGG TTGGATAAGG 300
20 ACATAACAGA AGCAATAGAG ACTACCATTA GTCTTGAAAC AGCACGTGCA GACCATCCGA 360
AGCCTGTAAC TGTGAAACCA GTAACAACGG AACCTCAGAG TCCAGATCTG AACGATGCCG 420
TGTCCAGTTT GCGAAGTCCT ATTCCCCTCC TCCTGTCGTG TGCCTTTGTT CAGGTGGGGA 480
25 TGTATTTTCA GTAGAAGGTG GAAGAAGGCT GCTATGACTC TTTGGATGGG AGTCTGGCAA 540
GAGGAAATG GAAGATAAAA TAAATAATAA GTGAAATAAA AAAAAAAAAA AAAAAGTCTGA 600
30 GGGGGGGCCC GGTACCCAAT 620

35 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

45 ACAAGGTGTG TGTAAGTTT ATGTTTGTA ACTGAATTCT ATCTTAAATC CAAAAAGAAC 60
TCGGGAGTAA TTCATTTTTG TAGCATAAAG ATCCCTAAGT TTTATTTTGA AATATCTGAT 120
TTTTACACGT TAAAAAATAA CAGGGCATCG AGAGGATTCC TAGGTGACAT CCAGACTCCT 180
50 TTAGCTTTGT GTGTGTGGCA CCGTTAGTC TGCTTCTCTC TCCTTTCTTG CACTGCTTCA 240
CACAGCCATG CCCTGCCAGC CCGGGCAGGT GCCTTCCTGT CAATGTACAT TTGGGCTTCT 300
55 GCTCATGCTG CCCTCCCTCC CCTCCCTGC CTCCAACCC CGCCCTTTT GTTCCTCCAT 360
GGAGTACTTC CATGGGTGTG CCTCCCCCAG CCAAGCCATA ATAGGTGGTT TCCCCTTCGC 420
TTCTGTAGCC CTTGCAGACA TCCTCTGTTT ACAGTAGGTG TTGACTTACT TCCCCTCTCC 480
60

CCGSTAAAGC CATAAACTCC TTAAGGACAG GTAGCATTCT TAGTATCTTC GTTCTTCTCA 540
 ATGACCAGTA GACCATTAAA CATGTAGCAA ACAAATGTGA A 581

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(2) INFORMATION FOR SEQ ID NO: 75:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1843 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

AAACCCAACN CCCTCCGGTC CCCNAAAGAA AGCCCAGCCC AAATCCCAAG CCGGCAGTGA 60
 20 GCCCGCGAAC AAGGCCCTCA AGACGCCCAG NCGAACAAGC AGCCCCCAGG AGGCCCCGCA 120
 AGAGAACTCC CTGGCGGCCC AAGCGGGCAG CTTCTGTGCG GCAGAACTCA GCCACCGAGA 180
 25 GCGCAGACAG CATCGAGATT TATGTCCCGG AGNCCCAGAC CAGGCTCTGA GACCATGCAG 240
 GAGGAAAGAA ACGATTTTAA ATCATTAATA ACACAAAAAC TAAGTGCGAA CGGAACAGAG 300
 TTTTCTCAAC CTTTGCTATG GTTATTCTGT CTAGAGACCC TGAGCCAACT TTCAAATTGA 360
 30 CGCATACAAG GGCTCACAAT TTGGCTTTTT TGGGTCCCTC CCAGCTTTAG GTTATGAAGA 420
 TTTTACTCAC AAAAAAATC AACAAAAATC ACGAACTAG AAAACTTTTT TTTTCTCTTT 480
 GCTGGCCGTG GTGGACTION TAGATGGACG TCGGCAACTC CCGGCCCAGC CTCCATACTG 540
 35 CGGTCTTTTT ACTCGTTCTA TCTGATGAGA ACTCACACTA GCTTGTTTAC AAGATGACGA 600
 CAGTCCAAGG GCAGCCTTGG GCACCTGCCA TGTCCCTCCT TTCCCCAGCT ATCCCCGCTC 660
 40 TGACCTTGAT TTTCATTCCT ATGTTTTTCT CTTTTCCCTT CAGAGCTCAC ACAGTGGTCA 720
 CCATTGTGGC AAGCGGCTTT CTGGGTCTCA GCCCTCTCTG CGGTGAGGG CCCAGAGGAC 780
 AGAGAGATGG ACATGCGTCC CCTCCCTCCC CCGCCAAGT GCTCACACAC AACCTCACGC 840
 45 GCACACACAC ACACGCAGAT GGAGGCGCCT CACTGGGAGG TGCCCCGCCA GCCCTGGGCA 900
 GTGTCAGGCA GGACTIONCTC ACCGCTGAGC AGATGAGAGA AGTTTTAGTC TTGGCGGGTG 960
 50 GAAATGAGAC GAAGCCACAG TTATCACACT CCAGACTCCT GCCCTTTTAT TTTCTCCAGC 1020
 CCCTTCTTCC TTCAGCAAAA TCTAGGACTC CCGAGTGGCT TCCAGGGGGC CGTCAGTCCT 1080
 CAGCCGCGCC TGTGTCCGGT GCCCGAGGGG CGGGCGGGG TGTCTGTATG TATGTGTACA 1140
 55 TATGCACATA GACCTTAGAG TGTATAGTTA ACAAACGCCC ATCTGCTCAC CCATGCCCCAC 1200
 CCAGCGCCGC CGCCGCTGGC TCTCGGGGCA CCTGGCAGGA GGCGGGTGTG TGAATAGCAT 1260
 60 ATATTTTTAC ATGTACTATA TCTAGGTGTG TGTACAAGTG TGTGTAAAAA TATATACCTT 1320

GTGTGTAAGC AGCCCTTTTT TTTTGGTTC TCCACCCCCC TCCCCCGCC CCGCACTCCT 1380
AAGGGCCCAT CTGCCAGCC TCTGAGTTT CTGTCTATT TTTTTTTAA CCCCATTAT 1440
5 CCTTCTCTCT CTCTGCCCC CGCATCCCAC TCCCAGGGTG TCACGAGCCC TGAGCTGCAA 1500
TGGCCCGGC CTGCAGGCG GGGTAGGGGA GGGCARGGCT SAGCCCCGAA GCCAGCTCAG 1560
10 TACCTGAGGG GCTGCTCTAT GCTGTGTATG CGCCTCTCTG GCATCCGAGA CATCCTCTTG 1620
GTGGCGCTTG CTNGCAGGGG ACCCCCCCCC CGTCCCCAGG TGAACCAAGG GTCTGCTCCG 1680
GGGCCCATT CCAGCTTGGC CGCCGTCTGT GACCTTGGGC AAGTCACTTG ACCTCTGTGT 1740
15 GCCTCAACTT CCTCTCTGT AAAACGGGGA CAGTCCCTGC CCCTCCCTAC CTCACAGGCA 1800
TGTGTGAGA ATAAATGAGG TAACGTGTAA AAAAAAAAAA AAT 1843
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(2) INFORMATION FOR SEQ ID NO: 76:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

TCGACCCACG CGTCCGGCTC CCCGAGCCCT GCCAACCATG GTGAACCTGG GTCTGTCCCG 60
35 GGTGGACGAC GCCGTGGCTG CCAAGCACCC GGGACTCGGG GAGTATGCCG CATGCCAGTC 120
ACACGCCTTC ATGAAGGGCG TTTTCACCTT CGTCACAGGC ACCGGCATGG CCTTTGGCTT 180
GCAGATGTTT ATTCAGAGGA AGTTTCCATA CCCTTTGCAG TGGAGCCTCC TAGTGGCCGT 240
40 GGTTCAGGC TCTGTGGTCA GCTACGGGGT GACGAGAGTG GAGTCGGAGA AATGCAACAA 300
CCTCTGGCTC TTCTGGAGA CCGGCAGCT CCCCAGAGC AGGAGCACAG ATCAGAGAAG 360
45 CTAGGAGAGC TCCAGCAGGG GCACAGAGGA TTGGGGGCAG GAGGAGTCTG GAACACAGCC 420
TTTCATGCCCC CTGACCCAG GCCGACCTC CCCACACCCT AGGGTACCC AGTCGTATCC 480
TCTGTCCGCA TGKTGGCCA GGCTGACAA ACACCTGCAG ATGGCTGCTG CCCCACCTG 540
50 GGACCTGCCC AGRAGGTGG AGCAGAAAGG GCTCTCCCTG GGGTGGTGT TCTCTCTAG 600
GGTATGGGA TGCATGTTCT GCACTGCCAG CAGAGAGGGT GTGTCTGGGG GCCACCACCT 660
55 ATGGGACACG GGGTCGAAGG GGCCTGTACA CTCTGTCATT TCCTTTCTAG CCCCTGCATC 720
TCCAACAAGT CCAAGGTGAC AGCTGGTGCT AGGGCGTGG GGTAAATAAA TGGCTTATCC 780
TTCTCTCCAC CCAAGTTTCC ACCTGACCAG GTGAAAAACA AATCAGAAGG GTAAGATGAT 840
60

	GACAGGTCAC ATGAAACCTT TATTACCTTA CAGTTGATAT ATGAGGATCA CATGCAAGTT	900
	ACATACTGAG GATGTACAGG GAAGTTCCCA GCGCTGAACC CCAGAATTAG ACGTTCGCAT	960
5	CAGCCCCGTA GGCCACGTGG ACACCACCAC AGCCTCTCTG TATGGGGGTC TGCCTCTGTA	1020
	GCACTTGCCA TGTAGGGGCA GAGCAAAAGG GGCCANGCTG GCCAGAGCCT GGCTGCTGGG	1080
10	NAGARGAGGG ACTTGTGGGS CACGCCACNT GCCTATCATT CCCAYTCAT CTATTAGCCA	1140
	AAGTCACTCC CCAGAGGCAG AGCTAGCCCG TTGTAGCCGT GTCTGTGTGG AGGGAAAGCT	1200
	TCTGAGTGGG CAAGCCTACA CACAGCCCCG AGCCCCAAGA GGAGGAAGAG GTGGAGACCA	1260
15	GACGGAACCT CCACAAGTCC ATCATGGTTA CAGCTGGCTT CCCC GCAGCA CCGAAGACCC	1320
	ACAGCATNGG CCCTGCTGCC CCCGACCCAG CTCAGCTGCC ANGCCTCACC TTGCCAGGAA	1380
20	TTGAAAGAAA GTTATTGAGT ACTAATTGGC CTCAGAGTNA CAGGAAGCTC AAGTTAAAGT	1440
	G	1441

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(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 910 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

35	GGCAGAGCTG GCCTTCGACT CGCTATGTCC ACTAACAATA TGTCGGACCC ACGGAGGCCG	60
	AACAAAGTGC TGAGGTGAGG ACCCCAGCGT CGTGGGCACG GGTTCGGGTT GTGGGTGTGG	120
40	ATCGGGGCCC TGGGAAGCGC CTGTCTATCC CGGGGCGAGG ACCTGAGCGC CCTGACCCT	180
	CGAGCCTGTC GCAGGTACAA GCCCCGCCG AGCGAATGTA ACCCGGCCTT GGACGACCCG	240
45	ACGCCGGA CT ACATGAACCT GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG	300
	CTGAAGTGGT GTGCTTGGGT CGCTGTCTAC TGCTCCTTCA TCAGCTTTGC CAACTCTCGG	360
	AGCTCGGAGG ACACGAAGCA AATGATGAGT AGCTTCATGT GAGACTTGCC CTACAGAACA	420
50	AGTGA CTCTT GAGTAAGGGG TGGGGGACC CCAGCCTGGC CATCCTAGAC TGACACCTCT	480
	CTCCTGTCTT CATGCTGTCC ATCTCTGCCG TGGTGATGTC CTATCTGCAG AATCCTCAGC	540
55	CCATGACGCC CCCATGGTGA TACCAGCCTA GAAGGGTCAC ATTTTGGACC CTGTCTATCC	600
	ACTAGGCCTG GGCTTTGGCT GCTAAACCTG CTGCCTTCAG CTGCCATCCT GGACTTCCCT	660
	GAATGAGGCC GTCTCGGTGC CCCCAGCTGG ATAGAGGGAA CCTGGCCCTT TCCTAGGGAA	720
60	CACCCTAGGC TTACCCCTCC TGCCTCCCTT CCCCTGCCTG CTGCTGGGGG AGATGCTGTC	780

CATGTTTCTA GGGGTATTCA TTGCTTTCT CGTTGAAACC TGTTGTTAAT AAAGTTTTC 840
 ACTCTGAAAA AAAAAAAAAA AAAAAAAC TYGRGGGGG GCCCGGAACC CAATTCSCCG 900
 5 GATAGTGAGT 910

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(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

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TCGACCCACG CGTCCGGGCG GGCAGTGATG GCGGCTGGTG ATGGGGACGT GAAGCTAGGC 60
 ACCCTGGGGA GTGGCAGCGA GAGCAGCAAC GACGGCGGCA GCGAGAGTCC AGGCGACGCG 120
 GGAGCGGCAG CGRAAGGGG AGGCTGGGCG GCGGCGGCGT TGGCGCTTCT GACGGGGGGC 180
 GGGGAAATGC TGCTGAACGT GCGGCTGGTG GCTCTGGTGC TGCTGGGGGC CTACCGGCTG 240
 TGGGTGCGCT GGGGGCGGCG GGGTCTGGGG GCCGGGGCCG GGGCGGGCGA GGAGAGCCCC 300
 GCCACCTCTC TGCCTCGCAT GAAGAAGCGG GACTTCAGCT TGGAGCAGCT GCGCCAGTAC 360
 GACGGCTCCC GCAACCCGCG CATCCTGCTC GCGGTCAATG GGAAAGTCTT CGACGTGACC 420
 AAAGGCAGCA AGTTCTACGG CCCGGCGGGT CCATATGGAA TATTTGCTGG TAGGGATGCC 480
 TCCAGAGGAC TGGCCACATT TTGCCTAGAT AAAGATGCAC TTAGAGATGA ATATGATGAT 540
 CTCTCAGATT TGAATGCAGT ACAAATGGAG AGTGTTCGAG AATGGGAAAT GCAGTTTAAA 600
 GAAAAATATG ATTATGTAGG CAGACTCCTA AAACCAGGAG AAGAACCATC AGAATATACA 660
 GATGAAGAAG ATACCAAGGA TCACAATAAA CAGGATTGAA CTTTGTAAC AACCAAAGTC 720
 AGGGGCCTTC AGAACTGCAA TTCTTACTCC CTTTCACAGA CTGTCCGAG TCTTTGGGTT 780
 TGATTACCT GCTGCGAAAA ACATTCAACA AATTGTGTAC AAGATAAATT AATCTCACTA 840
 TGAAGATTG AATAACTAGA CATTTATTAT GCTGCCAAAC TCATTTGTTG CAGTTGTTTG 900
 TAATGTCTAG TGGGGCTTCA TCATCTGAA AAGAAGGAGA CAGGGATTTT TTAAAGAGC 960
 AAGAAAGTCA CAATATTACT TCTTTCCTTC CTTTTTCCT TCTTTCCTT CTTCTTCTC 1020
 TTTCTTCTT TTAAATAT ATTGAAGACA ACCAGATATG TATTTGCTAC TCAAGTGAC 1080
 AGATCTCCTC AAGAAACATC AAGGGACTCC TGTGTCACAT ACTGTGTTT TATTTTAACA 1140
 TGGGTGAGGG AGGCGACCTG ATCAGGGGAG GTGGGGGTAC ACATCAATTT GAGTTGTTCA 1200

	GGCTACTGAA ACATTAAAAAT GTGAATTCCC AAACCTTTTCT TTTTGGCTTT GTCAGGGAAA	1260
	AGAAAAATAT CTTTATAAAG AAATCTTTGG AAATTAGGAG AAGGAATTTC AGGTGGGTTT	1320
5	AAGTCAGAGC TAGTTCCCCA ACAGAAAGAT CATTTGAAAC CAGTTTTTAT CCCTTCTCTT	1380
	TCCTTCCCTT TCCCTAAATC AAATCAATAT TAATTGTGCC TTATTTCAC TAAACATAGAC	1440
10	TTGAATTATT TTTAGGGAAA GCCCCTATAA TGAATTCAGA AATCACTACA AGCAGCATTA	1500
	AGACTGAAGT TGGAAATATC TGTGTGACCAT AAAACCTTGA TATCATCTCG TGTATATAGA	1560
	ATGTAAAAGG AATATTACAG TGTTAACTGC CATATATGTA ATATACACAA ACTCAATTAG	1620
15	CATTGTAATG GCCAAATGCA TTCCCCCATG CTTTCTGT TTTCAAAAAA TTGAAAAACA	1680
	AATCAACTCT TATCCCCAAC AGCTGCCTAA TTTTAGGAGT CTGACCCTCC ACATCTCACT	1740
20	GGTGTGGGTG CATGGGGCTG TGGAGTGGGT GTCAGTATGG ATGTGTCTGA ATGTGTGAGG	1800
	CCTTGAAGG GACTCTTTCT GCAGATACTG TAAATACAAG TACCATTTTA ATAAAGCATG	1860
	TACAATAAAC CAAAATAAGC TTGAGTTGGA CTTTATATAC AGAACTGTAA GCCAGTGCAT	1920
25	TATGATACAG TTGTAAGATT GTGCATTTGA TTCAAGATAA GGAAAAATCT TGGAAATGAA	1980
	AAGCAGGCAC KGGTTAACCA AGTTGTACAC ATTGTACCAC ATTCAGCATA ACTTTAGGAA	2040
30	GAAATTCAC TTTGTGAACA TTCTCCAGAA ATCCAAGATT ATTCAGGTAA GAATTGGTAT	2100
	ATTAAATGTA CATCTTTTTA CTTTCTATTT TGATGCCAAC TGATTATACT AGACAATTAG	2160
	CACTCCAGGT GGTATTGAA CACAAAACAG TAAAAGAATA TTGCACTGAT AGATACTAAA	2220
35	TTATTTATTTT ATTAGGTTGA AAAAGCCCTT ACTAAAAGCC CCTCATATAT CAATTACTTT	2280
	ATTTCAATTAT GACTACTTAG GTTCCGGGCT GGGGACAAGT TCACTTAAAA AGGCAATGTT	2340
40	ATTTAACAGG TCACCAGTTA AGACTTCTGC TTTGTAGATA CATGCAGAAG CCATCAAACA	2400
	AGGGGGRGCT TTAACTGCA ACAATAAGCT AAAGTATGTA AAATACTACA TTCTATTGAG	2460
	TCTTGGAGTG TTTTGTAGAA AGTTATCTTC AGCCAAATCT TTGCTGAAGA CTGGTTGTGG	2520
45	AGTGTGGTA AATGCTTTGT GTTTTATGT AAAATATTTT CTAAACAAAA AATGTTAAAA	2580
	GTACATGTCC TCTGTAGTAA ACTGATATCT ATATATATGA ATCATTCAG CCTAAAGTCT	2640
50	AGTAATAAAC TGTAATTGTG AATAGAGAAA CCCTAAATAT TCATGCAGWA AAAATTATGC	2700
	GGTCTGTAA GAAAAATGAG TAATTTGTGT TTTGGACTTG AAATAAACAG TGTCTGTAG	2760
55	ATAATTCCTC AACTTC	2776

(2) INFORMATION FOR SEQ ID NO: 79:

60 (i) SEQUENCE CHARACTERISTICS:

229

(A) LENGTH: 1525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

	CCGCTGCTGA TAACTATGGC ATCCCCCGGG CCTGCAGGAA TTCGGCACGG AGCTACGGCG	60
10	CCGCCTGGCT CCTGCTGNCA CCTGCAGGCT CGTCGCGGGT GGAGCCCACC CAAGACATCA	120
	GCATCAGCGA CCAGCTGGGG GGCCAGGACG TGCCCGTGT TCCCTGCTGG	180
15	TGGTGGGTGT CGGCGCCGTG TTCTCACTGC TATTCCACCT GGGCACCCGG GAGAGGCGCC	240
	GGCCGCATGC GGASGAGCCA GGCGAGCACA CCCCCCTGTT GGCCCCTGCC ACGGCCCAGC	300
	CCCTGCTGCT CTGGAAGCAC TGGCTCCGGG AGCSGGCTTT CTACCAGGTG GGCATACTGT	360
20	ACATGACCAC CAGGCTCATC GTGAACCTGT CCCAGACCTA CATGGCCATG TACCTCACCT	420
	ACTCGCTCCA CCTGCCCAAG AAGTTCATCG CGACCATTC CCTGGTGATG TACCTCAGCG	480
25	GCTTCTTGTC CTCCTTCCTC ATGAAGCCCA TCAACAAGTG CATTGGGAGG AACATGACCT	540
	ACTTCTCAGG CCTCCTGGTG ATCCTGGCCT TTGCCGCTG GGTGGCGCTG GCGGAGGGAC	600
	TGGGTGTGGC CGTGTACGCA GCGGCTGTGC TGCTGGGTGC TGGCTGTGCC ACCATCCTCG	660
30	TCACCTCGCT GGCCATGACG GCGACCTCA TCGGTCCCCA CACGAACAGC GGACTKTCGT	720
	GTACGGCTCC ATGAGCTTCT TGGATAAGGT GGCCAATGGG CTGGCAGTCA TGGCCATCCA	780
35	GAGCCTGCAC CTTTGCCCT CAGAGCTCTG CTGCAGGGCC TGCGTGAGCT TTTACCACTG	840
	GGCGATGGTG GCTGTGACGG GCGGCGTGGG CGTGGCCGCT GCCCTGTGTC TCTGTAGCCT	900
	CCTGCTGTGG CCGACCCGCC TCGACGCTG GGACCGTGAT GCGCGGCCCT GACTCCTGAC	960
40	AGCCTCCTGC ACCGTGTCAA GGGAACTGTG GGGACGCACG AGGATGCCCC CCARGGCCTT	1020
	GGGGAAGAGC CCCCCTGCC CCTCACTCTT CTCTGGACCC CCACCCTCCA TCCTCACCCA	1080
45	GCTCCCGGGG GTGGGGTCGG GTGAGGGCAG CAGGGATGCC CGCCAGGGAC TTGCAAGGAC	1140
	CCCCTGGGTT TTGAGGGTGT CCCATTCTCA ACTCTAATCC ATCCCAGCCC TCTGGAGGAT	1200
	TTGGGGTGCC CCTCTCGGCA GGGAACAGGA AGTAGGAATC CCAGAAGGGT CTGGGGGAAC	1260
50	CCTAACCCCTG AGCTCAGTCC AGTTCACCCC TCACCTCCAG CCTGGGGGTC TCCAGACACT	1320
	GCCAGGGCCC CCTCAGGACG GCTGGAGCCT GGAGGAGACA GCCACGGGGT GGTGGGCTGG	1380
55	GCCTGGACCC CACCGTGGTG GGCAGCAGGG CTGCCCCGCA GGCCTGGTGG ACTCTGCTGG	1440
	CAGCAAATAA AGAGATGACG GCAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1500
60	AAAAAAAAAA AAACCCACCG TCCGC	1525

(2) INFORMATION FOR SEQ ID NO: 80:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

	AATTCGGCAC GAGNCAGAAA CCTGCGGAAA ATGGTAGCGA TGGCGGCTGG GCCGAGTGGG	60
15	TGTCCTGGTGC CGCGCTTTGG GCTACGGTTG TTGTTGGCGA CTGTGCTTCA AGCGGTGTCT	120
	GCTTTTGGGG CAGAGTTTTT ATCGGAGGCA TGCAGAGAGT TAGGCTTTTC TAGCAACTTG	180
20	CTTTGCAGCT CTTGTGATCT TCTCGGACAG TTCAACCTGC TTCAGCTGGA TCCTGATTGC	240
	AGAGGATGCT GTCAGGAGGA AGCACAATTT GAAACCAAAA AGCTGTATGC AGGAGCTATT	300
	CTTGAAGTTT GTGGATGAAA ATTGGGAAGG TTCCCTCAAG TCCAAGCTTT TGTTAGGAGT	360
25	GATAAACCCA AACTGTTT CAG AGGACTGCAA ATCAAGTATG TCCGTGGTTC AGACCCTGTA	420
	TTAAAGCTTT TGGACGACAA TGGGAACATT GCTGAAGAAC TGAGCATTCT CAAATGGAAC	480
	ACAGACAGTG TAGAAGAATT CCTGAGTGAA AAGTTGGAAC GCATATAAAT CTTGCTTAAA	540
30	TTTTGTCTTA TCCTTTTGTG ACCTTATCAA ATGAAATATT ACAGCACCTA GAAAATAATT	600
	TAGTTTTGCT TGCTTCCATT GATCAGTCTT TTA CTGAGG CATTAAATAT CTAATTAAAT	660
35	CGTGAAATGG CAGTATAGTC CATGATATCT AAGGAGTTGG CAAGCTTAAC AAAACCCATT	720
	TTTTATAAAT GTCCATCCTC CTGCATTGTG TGATACCACT AACAAAATGC TTTGTAACAG	780
40	ACTTGGCGTT AATTATGCAA ATGATAGTTT GTGATAATTG GTCCAGTTT ACGAACAACA	840
	GATTTCTAAA TTAGAGAGGT TAACAAGACA GATGATTACT ATGCCTCATG TGCTGTGTGC	900
	TCTTTGAAAG GAATGACAGC AGACTACAAA GCAAATAAGA TATACTGAGC CTCAACAGAT	960
45	TGCCGTGCTCC TCAGAGTCTC TCCTATTTTT GTATTACCCA GCTTCTTTT TAATACAAAT	1020
	GTTATTTATA GTTTACAATG AATGCACTGC ATAAAACTT TGTAGCTTCA TTATTGTAAA	1080
50	ACATATTCAA GATCCTACAG TAAGAGTGAA ACATTCACAA AGATTGCGT TAATGAAGAC	1140
	TACACAGAAA ACCTTCTTAG GGATTGTGTG GGATCAGATA CATACTGGC AAATTTTGA	1200
	GTTTTACATT CTTACAGAAA AGTCCATTTA AAAGTGATCA TTTGTAAGAC CAAAATATAA	1260
55	ATAAAAAGTT TCAAAAATCT ATCTGAATTT GGAATTCCTC TGGTTGTGTC TTTTATGTTT	1320
	AAAAATGATG TTTTCAATG CATTTTTTTC ATGTAAGCCC TTTTTTTAGC CAAAATGTAA	1380
60	AAATGGCTGT AATATTTAAA ACTTATAACA TCTTATTGTT GGTAATAGTG CTTTATATTT	1440

GTCTGATTTT ATTTTTCAAA GTTTTTCAT TTATGAACAC ATTTTCATTG GTATATTATT 1500
TAAGGAATAT CTCTTGATAT AGAATTTTA TATTAAAAAT GATTTTCTT TGCTTAAAAA 1560
5 AAA 1563

10 (2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

20 TGCACGCTGG CCATGTGGGN GTTGGGCCAC TGCACCCCC GCGCTGCAC GGGCCGCAAG 60
CTGGCCCGCC TGGGCTGGT GCGCTGCCTG CGCTGGGCC ACAGATTCGG CGGTCTGGTG 120
CTGAGCCCCG TGGGCAAGCA GTACGCGTCC CCCGAGACA GACAGCTGGT GGCGCAGTCT 180
25 GGGGTCGCCG TCATCGACTG CTCCTGGGCC AGGCTGGACG AGACACCGTT TGGGAAGATG 240
CGAGGGAGCC ACTTGCGCCT GTTGCCCTAC CTGGTGGCCG CCAACCCCGT GAACTATGGC 300
30 CGGCCCTACA GACTTTCCTG CGTGAAGCG TTTGCTGCCA CCTTCTGCAT CGTAGGCTTT 360
CCAGACCTTG CTGTCATTTT GCTGCGGAAG TTAAATGGG GCAAGGGCTT CTTGACCTG 420
AACCGCCAGC TCCTGGACAA GTACGCGGCC TCGGCGAGCC CGGAGGAGGT GCTGCAGGCG 480
35 GAGCAGGAGT TCTTGGCCAA TGCCAAGGAG AGCCCCAGG AGGAGGAGAT CGATCCCTTC 540
GATGTGGATT CAGGGAGAGA GTTGGAAAC CCCAACAGGC CTGTGGCCAG CACCCGGCTG 600
40 CCCTCGGACA CTGATGACAG TGATGCGTCT GAGGACCCAG GGCCTKCGC CGAGCGCGGA 660
GGAGCCAGCA GCAGCTGCTG TGAAGAGGAG CAGACGCAGG GACGGGGGCG TGAGGCCAGG 720
GCCCCGGCTG AGGTTTGGAA AGGAATCAAG AAACGCGAGA GAGACTGAGG GTTGCAGACA 780
45 CATATATTTT TGAGGCTGGG TGACGAGAAA ATCTAGAGAC ATGAGGGACA TAAATGGGCC 840
TGGCAGCCTC GGCTCTTTC GGCTGCTGGC AGGACTGAGC TGTCCGGGTT CTCCCACAC 900
50 TTCCAGCACA GCTGTGCTCT GTGCTCTGCC TCGGCGCTCT CGCAAATGAA GCTGCAGGCC 960
AAGAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAG GGGGGGGGC 1020

55

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 770 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

	TCGACCCACG CGTCCGGGCC GCCGTAGCGC GTCTTGGGTC TCCCGGCTGC CGCTGCTGCC	60
10	GCCGCCGCCT CGGGTCGTGG AGCCAGGAGC GACGTCACCG CCATGGCAGG CATCAAAGCT	120
	TTGATTAGTT TGTCTTTTGG AGGAGCAATC GGACTGATGT TTTTTRATGCT TGGATGTGCC	180
	CTTCCAATAT ACAACAAATA CTGGCCCCCTC TTTGTTCTAT TTTTTTACAT CCTTTCACCT	240
15	ATTCCATACT GCATAGCAAG AAGATTAGTG GATGATACAG ATGCTATGAG TAACGCTTGT	300
	AAGGAACTTG CCATCTTTCT TACAACGGGC ATTGTCGTGT CAGCTTTTGG ACTCCCTATT	360
	GTATTTGCCA GAGCACATCT GATTGAGTGG GGAGCTTGTG CACTTGTTCT CACAGGAAAC	420
20	ACAGTCATCT TTGCAACTAT ACTAGGCTTT TTCTTGGTCT TTGGAAGCAA TGACGACTTC	480
	AGCTGGCAGC AGTGGTGAAA AGAAATTACT GAACTATTGT CAAATGGACT TCCTGTCAAT	540
25	TGTTGGCCAT TCACGCACAC AGGAGATGGG GCAGTTAATG CTGAATGGTA TAGCAAGCCT	600
	CTTGGGGGTA TTTTAGGTGC TCCCTTCTCA CTTTATTGT AAGCATACTA TTTTCACAGA	660
	GACTTGCTGA AGGATTAAAA GGATTTTCTC TTTTGAAAA AAAAAAAAAA AAAAACYCGA	720
30	GGGGGGGCCC GTWCCCATTC SCCCATATG AATTCCNTT TTACAATCCC	770

35 (2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

	GAATTCGGCA CGAGCATAGT GTTAACCACT AGAATTCACCT GCCCTTCCTA TCCAAAAATG	60
	ACACTACTGA TCATTTTCTC TCCTTTTCTC TTTACAACAT TMACAAATTC AGGTGGCTCT	120
50	TTCCCAGTAC GGTAGGCTGA TTCGTATGGA TGCACCACGG TTGGTGACTC CCCCCACCCC	180
	ACAGAGTTTC TGGCGTTCAT TCGGTTGAAC CCAAGGCCAG CAAGGGCTGA CTGGGAACAA	240
55	ACCGAACACT AGGCCGTGAA CCAATCGTCT CTCCGTGCCC GGGAGCGAMC CCGGGGGCCT	300
	TTCACTCTCC CAAGGACTCC ANGGGGGGGC CGGGTACCCA ATTCCGCCCC TATAGTGAAT	360
	CCGTNATTAC AATTCCACNT GGGCCGTCCN TTTTACAAA CGTTCCGTTG AACTGGGAAA	420
60	AACCCCTTGG CGGTTTACCC CAACTTTAAT CCGCCTTTC AAGCACATCC CCCCCCTTTT	480

C

481

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(2) INFORMATION FOR SEQ ID NO: 84:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 644 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

20

GCTGGGATAG AGCATGAAAG GAGAACTGCT CCCTTTTCTG TTTCTCACAG TTTGGTTATG 60

GCTTTATAAA CTTKTATTTG GTGAAAGCCC CAGATACCCA AATGTCATTG GCAAAACTTA 120

TTTTTTTTTC TGGACAGATC AGATTCTAG AGAGAGCAGA TTTCTAGAGA GATTAGCATT 180

CATAGTAAGT GAAAATTGTC TAATTTTTTT AATCCATGCT ATTACTGGGC AGTAGGTCTA 240

25

ATTTTTTTTG ACAAAAAATA GATCTATTTT CCTTATATAT TGATTTAGAA TCTTAAGTTA 300

GAATTTTATA GAAGAAATGT CTGAGCAGTT CTATGTATGG AGGAGCAATT CAGCTTTTCA 360

30

GCAGCAACTT TATCTTTTGC CACTAGAGGG AGATCTGTGG TTGCTTTCTC CTTTGGAGAA 420

TAGCTGCTTT GCTTTTATTT TTAATTCTTA AGGTGGAAT AGAACTTATT CTCAAAATTC 480

CTTTAGTGTT ATTAAATATT TTCATTATT AGTCAAAGGT AAGTTAATTA AGCTTGTTTA 540

35

ATGATGCCAA TCTTATGCTT TTCTGTAATC TTCAATTTTT AATAAATGTG AGTTAGATAC 600

TAAGTGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 644

40

(2) INFORMATION FOR SEQ ID NO: 85:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1351 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GGCACGAGTG CGCASGCGTG GGGCTCTCTC CTTGTCTAGTC GGCGCCGCGT GCGGGCTGGT 60

55

GGCTCTGTGG CAGCGGCGGC GGCAGGACTC CGGCACTATG AGCGGCTTCA GCACCGAGGA 120

GCGCGCCGCG CCNTTCTCCC TGGAGTACCG AGTCTTCCTC AAAAATGAGA AAGGACAATA 180

TATATCTCCA TTTCATGATA TTCCAATTTA TGCAGATAAG GATGTGTTTC ACATGGTAGT 240

60

TGAAGTACCA CGCTGGTCTA ATGCAAAAAT GGAGATTGCT ACAAAGGACC CTTTAAACCC 300

5 TATTAAACAA GATGTGAAAA AAGGAAAAC TCGCTATGTT GCGAATTTGT TCCCGTATAA 360
 AGGATATATC TGGAACATATG GTGCCATCCC TCAGACTTGG GAAGACCCAG GGCACAATGA 420
 TAAACATACT GGCTGTTGTG GTGACAATGA CCCAATTGAT GTGTGTGAAA TTGGAAGCAA 480
 GGTATGTGCA AGAGGTGAAA TAATTGGCGT GAAAGTTCTA GGCATATTGG CTATGATTGA 540
 10 CGAAGGGGAA ACCGACTGGA AAGTCATTGC CATTAATGTG GATGATCCTG ATGCAGCCAA 600
 TTATAATGAT ATCAATGATG TCAAACGGCT GAAACCTGGC TACTTAGAAG CTACTGTGGA 660
 CTGGTTTAGA AGGTATAAGG TTCTTGATGG AAAACCAGAA AATGAGTTTG CGTTTAATGC 720
 15 AGAATTTAAA GATAAGGACT TTGCCATTGA TATTATTAAA AGCACTCATG ACCATTGGAA 780
 AGCATTAGTG ACTAAGAAAA CGAATGGAAA AGGAATCAGT TGCATGAATA CAACTTTGTC 840
 20 TGAGAGCCCC TTCAAGTGTG ATCCTGATGC TGCCAGAGCC ATTGTTGGATG CTTTACCACC 900
 ACCCTGTGAA TCTGCCTGCA CAGTACCAAC AGACGTGGAT AAGTGGTTCC ATCACCAGAA 960
 AACTAATGA GATTTCTCTG GAATACAAGC TGATATTGCT ACATCGTGTT CATCTGGATG 1020
 25 TATTAGAAGT AAAAGTAGTA GCTTTTCAAA GCTTTAAATT TGTAGAACTC ATCTAACTAA 1080
 AGTAAATCTT GCTGTGACTA ATCCAATATA CTCAGAATGT TATCCATCTA AAGCATTTTT 1140
 30 CATATCTCAA CTAAGATAAC TTTTAGCACA TGCTTAAATA TCAAAGCAGT TGTCATTTGG 1200
 AAGTCACTTG TGAATAGATG TGCAAGGGGA GCACATATTG GATGTATATG TTACCATATG 1260
 TTAGGAAATA AAATTATTTT GCTGAAAAAA AAAAAAAAAA AACCNCGGGG GGGGCCCCGG 1320
 35 TCCCCATTG GCCCTTTGGG GGGNGGTTTT A 1351

40

(2) INFORMATION FOR SEQ ID NO: 86:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2527 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CTCTTGCTAC CTTCCCGGCG CAGAGAACCC CGGCTGCTCA GCGCGCTCCG GGGTCATGGA 60
 GATCCCCGGG AGCCTGTGCA AGAAAGTCAA GCTGAGCAAT AACGCGCAGA ACTGGGGAAT 120
 55 GCAGAGAGCA ACCAATGTCA CCTACCAAGC CCATCATGTC AGCAGGAACA AGAGAGGTCA 180
 GGTGGTGGGG ACCAGAGGTG GCTTTCGTGG TTGCACAGTT TGGCTAACAG GCTTGTCTGG 240
 AGCGGGAAAG ACTACTGTGA GCATGGCCTT GGAGGAGTAC CTGGTTTGTC ATGGTATTCC 300
 60

	ATGCTACACT CTGGATGGTG ACAATATTCG TCAAGGTC TC AATAAAAATC TTGGCTTTAG	360
	TCCTGAAGAC AGAGAAGAGA ATGTTTCGACG CATCGCAGAA GTTGCTAAAC TGTTTGAGAGA	420
5	TGCTGGCTTA GTGTGCATCA CAAGTTTCAT ATCACCTTAC ACTCAGGATC GCAACAATGC	480
	AAGGCAAAT CATGAAGGTG CAAGTTTACC GTTTTGTGAA GTATTTGTTG ATGCTCCTCT	540
10	GCATGTTTGT GAACAGAGGG ATGTCAAAGG ACTCTACAAA AAAGCCCGGG CAGGAGAAAT	600
	TAAAGGTTTC ACTGGGATCG ATTCTGAATA TGAAAAGCCA GAGGCCCTG AGTTGGTGCT	660
	GAAAACAGAC TCCTGTGATG TAAATGACTG TGTCCAGCAA GTTGTTGGAAC TTCTACAGGA	720
15	ACGGGATATT GTACCTGTGG ATGCATCTTA TGAAGTAAAA GAACTATATG TGCCAGAAAA	780
	TAAACTTCAT TTGGCAAAAA CAGATGCGGA AACATTACCA GCACTGAAAA TTAATAAAGT	840
20	GGATATGCAG TGGGTGCAGG TTTTGGCAGA AGGTTGGGCA ACCCCATTGA ATGGCTTTAT	900
	GAGAGAGAGG GAGTACTTGC AGTGCCTTCA TTTTGATTGT CTCTGATG GAGGTGTCAT	960
	TAACTTGTC GTACCTATAG TTCTGACTGC GACTCATGAA GATAAAGAGA GGCTGGACGG	1020
25	CTGTACAGCA TTTGCTCTGA TGTATGAGGG CCGCGGTGTG GCCATTCTTC GCAATCCAGA	1080
	GTTTTGTGAG CACAGGAAAG AGGAGCGCTG TGCCAGACAG TGGGGAACGA CATGCAAGAA	1140
30	CCACCCCTAT ATTAAGATGG TGATGGAACA AGGAGATTGG CTGATTGGAG GAGATCTTCA	1200
	AGTCTTGAT CGAGTTTATT GGAATGATGG TCTTGATCAG TATCGTCTTA CTCCTACTGA	1260
	GCTAAAGCAG AAATTTAAAG ATATGAATGC TGATGCTGTC TTTGCATTTC AACTACGCAA	1320
35	CCCAGTGCAC AATGGACATG CCCTGTTAAT GCAGGATACC CATAAGCAAC TTCTAGAGAG	1380
	GGGCTACCGG CGCCCTGTCC TCCTCCTCCA CCCTCTGGGT GGCTGGACAA AGGATGACGA	1440
40	TGTTCTTTTG ATGTGGCGTA TGAAGCAGCA TGCTGCAGTG TTGGAGGAAG GAGTTCTGAA	1500
	TCCTGAGACG ACAGTGGTGG CCATCTTCCC ATCTCCCATG ATGTATGCTG GACCAACTGA	1560
	GGTCCAGTGG CATTGCAGAG CACGGATGGT TGCAGGAGCC AACTTTTACA TTGTTGGACG	1620
45	AGACCCTGCT GGCATGCCTC ATCCAGAAAC AGGGAAGGAT CTTTATGAGC CAAGTCATGG	1680
	TGCCAAAGTG CTGACGATGG CCCCTGGTTT AATCACTTTG GAAATAGTTC CCTTTGAGT	1740
50	TGCAGCTTAC AACAAGAAAA AGAAGCGTAT GGACTACTAT GACTCTGAAC ACCATGAAGA	1800
	CTTTGAATTT ATTTAGGAA CACGAATGCG CAACTTGCT CGAGAAGGCC AGAAACCACC	1860
	TGAAGGTTTC ATGGCTCCCA AGGCTTGGAC CGTGCTGACA GAATACTACA AATCCTTGGA	1920
55	GAAAGCTTAG GCTGTTAACC CAGTCACTCC ACCTTTGACA CATTACTAGT AACAAGAGGG	1980
	GACCACATAG TCTCTGTTGG CATTTCTTTG TGGTGTCTGT CTGGACATGC TTCCTAAAAA	2040
60	CAGACCATTT TCCTTAACCT GCATCAGTTT TGGTCTGCCT TATGAGTTCT GTTTTGAACA	2100

AGTGTAACAC ACTGATGGTT TTAATGTATC TTTTCCACTT ATTATAGTTA TATTCCTACA 2160
 ATACAATTTT AAAATTGTCT TTTTATATTA TATTTATGCT TCTGTGTCAT GATTTTTTCA 2220
 5 AGCTGTTATA TTAGTTGTAA CCAGTAGTAT TCACATTAAA TCTTGCTTTT TTTCCCTTA 2280
 AAAAAAGAAA AAAATTACCA AACAATAAAC TTGGCTAGAC CT'TGT'TTGA GGATT'TTACA 2340
 10 AGACCTTTGT AGCGATTAGA TTT'TTTTCT ACATTGAAAA TAGAACTGC TTCCT'TTCTT 2400
 CTTTCCAGTC AGCTATTGGT CTTTCCAGCT GTTATAATCT AAAGTATTCT TATGATCTGT 2460
 GTAAGCTCTG AATGAACTTC TTTACTCAAT AAAATTAATT TTTTGGCTTC TTAAAAAAA 2520
 15 AAAAAA 2527

20 (2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2566 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

30 CCCAAGAATT CGGCACGAGC GNGGCAWAAK TGGGATTTCT GAAACCTGTA GGCCCCAAGC 60
 CCATCAACTT GCCCAAAGAA GATTCCAAAC CTACATTTCC CTGGCCTSCT GGAAACAAGC 120
 CATCTCTTCA CAGTGTA AAC CAAGACCATG ACTTAAAGCC ACTAGGCCGA AATCTGGGCC 180
 35 TACTCTCCA ACCTCAGAAA ATGAACAGAA GCAAGCKTTT CCCAAATTGA CTGGGGTTAA 240
 AGGGAAATTT ATGTCAGCAT CACAAGATCT TGAACCCAAG CCCCTCTTCC CCAAACCCGC 300
 40 CTTTGGCCAG AAGCCGCCCC TAAGTACCGA GAACTCCCAT GAAGACGAAA GCCCATGAA 360
 GAATGTGTCT TCATCAAAAG GGTCCCCAGC TCCCCTGGGA GTCAGGTCCA AAAGCGGCCC 420
 TTTAAACCA GCAAGGAAG ACTCAGAAAA TAAAGACCAT GCAGGGGAGA TTTCAAGTTT 480
 45 GCCCTTTCTT GGAGTGGTTT TGAAACCTGC TGCGAGCAGG GGAGGCCAG GTCTCTCAA 540
 AAATGGTGAA GAAAAAAGG AAGATAGGAA GATAGATGCT GCTAAGAACA CCTTCCAGAG 600
 50 CAAAATAAAT CAGGAAGAGT TGGCTCAGG GACTCTCTCT GCCAGGTTCC CTAAGGCCCC 660
 TTCTAAGCTG ACAGTGGGGG GGCCATGGGG CCAAAGTCAG GAAAAGGAAA AGGGAGACAA 720
 GAATTCAGCC ACCCCGAAAC AGAAGCCATT GCCTCCCTTG TTTACCTTGG GTCCACCTCC 780
 55 ACCAAAACCC AACAGACCAC CAAATGTTGA CCTGACGAAA TTCCACAAAA CCTCTTCTGG 840
 AAACAGTACT AGCAAAGGCC AGACGTCTTA CTCAACAAC TCCCTGCCAC CACCTCCACC 900
 60 ATCCCATCCG GCCAGCCAAC CACCATTGCC AGCATCTCAC CCATCACAAC CACCAGTCCC 960

	AAGCCTACCT CCCAGAAACA TTAAACCTCC GTTTGACCTA AAAAGCCCTG TCAATGAAGA	1020
	CAATCAAGAT GGTGTCACGC ACTCTGATGG TGCTGGAAAT CTAGATGAGG AACAGACAG	1080
5	TGAAGGAGAA ACATATGAAG ACATAGAAGC ATCCAAAGAA AGAGAGAAGA AAAGGGAAAA	1140
	GGAAGAAAAG AAGAGGTTAG AGCTGGAGAA AAAGGAACAG AAAGAGAAAG AAAAGAAAGA	1200
10	ACAAGAAATA AAGAAGAAAT TTAAACTAAC AGGCCCTATT CAAGTCATCC ATCTTGCAAA	1260
	AGCTTGTTGT GATGTCAAAG GAGGAAAGAA TGAAGTGAAG TTCAAGCAAG GAGAGCAAAT	1320
	TGAAATCATC CGCATCACAG ACAACCCAGA AGGAAAATGG TTGGGCAGAA CAGCAAGGGG	1380
15	TTCATATGGC TATATPAAAA CAACTGCTGT AGAGATTGAC TATGATTCTT TGAAACTGAA	1440
	AAAAGACTCT CTTGGTGCCC CTTCAAGACC TATTGAAGAT GACCAAGAAG TATATGATGA	1500
20	TGTTGCAGAG CAGGATGATA TTAGCAGCCA CAGTCAGAGT GGAAGTGGAG GGATATTCCC	1560
	TCCACCACCA GATGATGACA TTTATGATGG GATTGAAGAG GAAGATGCTG ATGATGGCTC	1620
	CACACTACAG GTTCAAGAGA AGAGTAATAC GTGGTCCTGG GGGATTTTGA AGATGTTAAA	1680
25	GGGAAAAGAT GACAGAAAGA AAAGTATACG AGAGAAACCT AAAGTCTCTG ACTCAGACAA	1740
	TAATGAAGGT TCATCTTTCC CTGCTCCTCC TAAACAATTG GACATGGGAG ATGAAGTTTA	1800
30	CGATGATGTG GATACCTCTG ATTTCCCTGT TTCATCAGCA GAGATGAGTC AAGGAACTAA	1860
	TGTTGGAAAA GCTAAGACAG AAGAAAAGGA CCTTAAGAAG CTAAAAAGC AGRAAAAARA	1920
	ARAAAAAGAC TTCAGGAAAA AATTFAAATA TGATGGTGAA ATTAGAGTCC TATATTCAAC	1980
35	TAAAGTTACA ACTTCCATAA CTTCTAAAAA GTGGGGAACC AGAGATCTAC AGGTAAAACC	2040
	TGGTGAATCT CTAGAAGTTA TACAAACCAC AGATGACACA AAAGTTCTCT GCAGAAATGA	2100
40	AGAAGGGAAT TATGGTTATG TCCTTCGGAG TTACCTAGCG GACAATGATG GAGAGATCTA	2160
	TGATGATATT GCTGATGGCT GCATCTATGA CAATGACTAG CACTCAACTT TGGTCATTCT	2220
	GCTGTGTTCA TTAGGTGCCA ATGTGAAGTC TGGATTTTAA TTGGCATGTT ATTGGGTATC	2280
45	AAGAAAATTA ATGCACAAAA CCACTTATTA TCATTTGTTA TGAAATCCCA ATTATCTTTA	2340
	CAAAGTGTTC AAAGTTTGAA CATAGAAAAT AATCTCTCTG CTTAATTGTT ATCTCAGAAG	2400
50	ACTACATTAG TGAGATGTAA GAATTATTAA ATATTCCATT TCCGCTTTGG CTACAATTAT	2460
	GAAGAAGTTG AAGGTACTTC TTTTAGACCA CCAGTAAATA ATCCTCCTTC AAAAAATAAA	2520
55	AATAAAAAAA AAAAAAAA ACTCGAGGGG GGGCCCGGTA CCAAT	2566

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

10 GAATTCGGCA CGAGGCTTTC TGTGTCCTCT GTGGCTGCTT TAGTGTGCCA CCAGGGGCAG 60
 ACTTGGGTGG GTTGCAGCAG AGATGGCATG GCCCTCAAGG TCCAAGATGT TTA CTCTCTT 120
 GCCGGTCCTC TGTTATCTCT GGTCTTTGTG GTTGCCACAG TTTTCTTGGA TCCAGGAGTT 180
 15 AAAGGCAGTC CTGAGGGATG ATGGCCTCAT CTCCGCAGTT GCYTGGAATG CTGAATTTC A 240
 GACGTGCTAA AGGAGGGTTG CAGACATTGT GTGGWATGCA TTCAGACCCC AGATGTGGGT 300
 GCAGGAAGGC AGGCATGGCA CAGCCAGGTA GAGACTGGTT TCCAGGCCCA AGCAGCCTTC 360
 20 AGCAGCTGTG CGCCTTGTTT CTGATGTTGT TTGGGAGTAA GAATAATGTA GACATGGGGG 420
 GTCATGARGC TCAATAAAAA CTCAAGGAA ACCTCCCATG GCATGGTTGG GCGCAGTGAC 480
 25 TCATGCCTGT AACCCAGCA CTGTGGAATG CCAAGGTGGA AGGATCGCTT GAGGCCAAGA 540

30 (2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1863 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

40 TCGACCCACG CGTCCGGCGA GATCCCTACC GCAGTAGCCG CCTCTGCCGC CGCGGAGCTT 60
 CCCGAACCTC TTCAGCCGCC CGGAGCCGCT CCCGGAGCCC GGCCGTAGAG GCTGCAATCG 120
 CAGCCGGGAG CCCGCAGCCC GCGCCCCGAG CCCGCCGCCG CCCTTCGAGG GCGCCCCAGG 180
 45 CCGCGCCATG GTGAAGGTGA CGTTCAACTC CGCTCTGGCC CAGAAGGAGG CCAAGAAGGA 240
 CGAGCCCAAG AGCGGCGAGG AGGCGCTCAT CATCCCCC GACGCCGTCG CGGTGGACTG 300
 50 CAAGGACCCA GATGATGTGG TACCAGTTGG CCAAAGAAGA GCCTGGTGTG GGTGCATGTG 360
 CTTTGGACTA GCATTTATGC TTGCAGGTGT TATTCTAGGA GGAGCATACT TGTACAAATA 420
 TTTTGCAC TT CAACCAGATG ACGTGTA CTA CTGTGGAATA AAGTACATCA AAGATGATGT 480
 55 CATCTTAAAT GAGCCCTCTG CAGATGCCCC AGCTGCTCTC TACCAGACAA TTGAAGAAAA 540
 TATTAAATC TTTGAAGAAG AAGAAGTTGA ATTTATCAGT GTGCCTGTCC CAGAGTTTGC 600
 60 AGATAGTGAT CCTGCCAACA TTGTTTCATGA CTTTAACAAG AACTTACAG CCTATTTAGA 660

5 TCTTAACCTG GATAAGTGCT ATGTGATCCC TCTGAACACT TCCATTGTGA TGCCACCCAG 720
 AAACCTACTG GAGTTACTTA TTAACATCAA GGCTGGAACC TATTTGCCTC AGTCCTATCT 780
 GATTCATGAG CACATGGTTA TTACTGATCG CATTGAAAAC ATTGATCACC TGGGTTTCTT 840
 TATTTATCGA CTGTGTCATG ACAAGGAAAC TTACAACTG CAACGCAGAG AACTATTAA 900
 10 AGGTATTCAG AAACGTGAAG CCAGCAATTG TTTCGCAATT CGGCATTTTG AAAACAAATT 960
 TGCCGTGGAA ACTTTAATTT GTTCTTGAAC AGTCAAGAAA AACATTATTG AGGAAAATTA 1020
 ATATCACAGC ATAACCCAC CCTTTACATT TTGTGCAGTG ATTATTTTTT AAAGTCTTCT 1080
 15 TTCATGTAAG TAGCAAACAG GGCTTTACTA TCTTTTCATC TCATTAATTC AATTAAAACC 1140
 ATTACCTTAA AATTTTTTTC TTTGGAAGTG TGGTGTCTTT TATATTTGAA TTAGTAAGTG 1200
 20 TATGAAGTCA TAGATAATAG TACATGTCAC CTTAGGTAGT AGGAAGAATT ACAATTTCTT 1260
 TAAATCATTT ATCTGGATTT TTATGTTTTA TTAGCATTTT CAAGAAGACG GATTATCTAG 1320
 AGAATAATCA TATATATGCA TACGTAAAAA TGGACCACAG TGACTTATTT GTAGTTGTTA 1380
 25 GTTGCCTGAC TACCTAGTTT GTTAGTGCAT TTGAGCACAC ATTTTAATTT TCCTCTAATT 1440
 AAAATGTGCA GTATTTTCAG TGTCAAATAT ATTTAACTAT TTAGAGAATG ATTTCCACCT 1500
 30 TTATGTTTTA ATATCCTAGG CATCTGCTGT AATAATATTT TAGAAAATGT TTGGAATTTA 1560
 AGAAATAACT TGTGTTACTA ATTTGTATAA CCCATATCTG TGCAATGGAA TATAAATATC 1620
 ACAAAGTTGT TTAAGTAGAC TGCCTGTTGT TTTCCCGTA TAATAAAACC AAAGAATAGT 1680
 35 TTGGTTCTTC AAATCTTAAG AGAATCCACA TAAAGAAGA AACTATTTTT TAAAAATCA 1740
 CTTCTATATA TACAATGAGT AAAATCACAG ATTTTTTCTT TAAATAAAAA TAAGTCATTT 1800
 40 TAATAACTAA ACCAGATTCT TTGTGATACT ATTAANGTAA CATTTAGCCC CAAAAAATAA 1860
 AAA 1863

45

(2) INFORMATION FOR SEQ ID NO: 90:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

60 GGCACAGCGG CACGAGGTGA GCTGAGCCGG TGGGTGAGCG GCGGCCACGG CATCCTGTGC 60
 TGTGGGGGCT ACGAGGAAAG ATCTAATTAT CATGGACCTG CGACAGTTTC TTATGTGCCT 120

	GTCCCTGTGC ACAGCCTTTG CCTTGAGCAA ACCCACAGAA AAGAAGGACC GTGTACATCA	180
	TGAGCCTCAG CTCAGTGACA AGGTTACAA TGATGCTCAG AGTTTTGATT ATGACCATGA	240
5	TGCCTTCTTG GGTGCTGAAG AAGCAAAGAC CTTTGATCAG CTGACACCAG AAGAGAGCAA	300
	GGAAAGGCTT GGAAAGATTG TAAGTAAAT AGATGGCGAC AAGGACGGGT TTGTCACTGT	360
10	GGATGAGCTC AAAGACTGGA TTAAATTTGC ACAAAGCGC TGGATTTACG AGGATGTAGA	420
	GCGACAGTGG AAGGGCATG ACCTCAATGA GGACGGCCTC GTTTCCTGGG AGGAGTATAA	480
	AAATGCCACC TACGGCTACG TTTTAGATGA TCCAGATCCT GATGATGGAT TTAACATAA	540
15	ACAGATGATG GTTAGAGATG AGCGGAGGTT TAAATGGCA GACAAGGATG GAGACCTCAT	600
	TGCCACCAAG GAGGAGTTCA CAGCTTTCCT GCACCCTGAG GAGTATGACT ACATGAAAGA	660
20	TATAGTAGTA CAGGAAACAA TGGAAGATAT AGATAAGAAT GCTGATGGTT TCATTGATCT	720
	AGAAGAGTAT ATTGGTGACA TGTACAGCCA TGATGGGAAT ACTGATGAGC CAGAATGGGT	780
	AAAGACAGAG CGAGAGCAGT TTGTTGAGTT TCGGGATAAG AACCGTGATG GGAAGATGGA	840
25	CAAGGAAGAG ACCAAAGACT GGATCCTTCC CTCAGACTAT GATCATGCAG AGGCAGAAGC	900
	CAGGCACCTG GTCTATGAAT CAGACCAAAA CAAGGATGGC AAGCTTACCA AGGAGGAGAT	960
30	CGTTGACAAG TATGACTTAT TTGTTGGCAG CCAGGCCACA GATTTTGGGG AGGCCTTAGT	1020
	ACGGCATGAT GAGTTCTGAG CTRCGGAGGA ACCCTCATTT CCTCAAAAGT AATTTATTTT	1080
	TACAGCTTCT GGTTCACAT GAAATTGTTT GCGCTACTGA GACTGTTACT ACAAACTTTT	1140
35	TAAGACATGA AAAGGCGTAA TGAAAACCAT CCCGTCCCCA TTCCTCCTCC TCTCTGAGGG	1200
	ACTGGAGGGA AGCCGTGCTT CTGAGGAACA ACTCTAATTA GTACACTTGT GTTTGTAGAT	1260
40	TTACACTTTG TATTATGTAT TAACATGGCG TGTTTATTTT TGTATTTTTC TCTGGTTGGG	1320
	AGTATGATAT GAAGGATCAA GATCCTCAAC TCACACATGT AGACAAACAT TAGCTCTTTA	1380
	CTCTTTCTCA ACCCCTTTTA TGATTTTAAT AATCTCACT TAACTAATTT TGTAAGCCTG	1440
45	AGATCAATAA GAAATGTTCA GGAGAGAGGA AAGAAAAAA ATATATGCTC CACAATTTAT	1500
	ATTTAGAGAG AGAACACTTA GTCTTGCCCTG TCAAAAAGTC CAACATTTCA TAGGTAGTAG	1560
50	GGGCCACATA TTACATTCAG TTGCTATAGG TCCAGCAACT GAACCTGCCA TTACCTGGGC	1620
	AAGGAAAGAT CCCTTTGCTC TAGGAAAGCT TGGCCCAAAT TGATTTTCTT CTTTTTCCCC	1680
	CTGTAGGACT GACTGTTGGC TAATTTTGTC AAGCACAGCT GTGGTGGGAA GAGTTAGGGC	1740
55	CAGTGTCTTG AAAATCAATC AAGTAGTGAA TGTGATCTCT TTGCAGAGCT ATAGATAGAA	1800
	ACAGCTGGAA AACTAAAGGA AAAATACAAG TGTTTTCGGG GCATACATTT TTTTCTGGG	1860
60	TGTGCATCTG TTGAAATGCT CAAGACTTAA TTATTTGCCT TTTGAAATCA CTGTAAATGC	1920

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CCCCATCCGG	TTCCTCTTCT	TCCCAGGTGT	GCCAAGGAAT	TAATCTTGGT	TTCAC TACAA	1980
TTAAAATTCA	CTCCTTTCCA	ATCATGTCAT	TGAAAGTGCC	TTTAACGAAA	GAAATGGTCA	2040
CTGAATGGGA	ATTCTCTTAA	GAAACCCTGA	GATTAAAAAA	AGACTATTTG	GATAACTTAT	2100
AGGAAAGCCT	AGAACCTCCC	AGTAGAGTGG	GGATTTTTTT	CTTCTTCCCT	TTCTCTTTTG	2160
GACAAAGTGT	AAATTAGCAG	TATTAGTTAT	GAGTTTGGTT	GCAGTGTCTT	TATCTTGTGG	2220
GCTGATTTCC	AAAAACCACA	TGCTGCTGAA	TTTACCAGGG	ATCCTCATAC	CTCACAATGC	2280
AAACCACTTA	CTACCAGGCC	TTTTTCTGTG	TCCACTGGAG	AGCTTGAGCT	CACACTCAAA	2340
GATCAGAGGA	CCTACAGAGA	GGGCTCTTTG	GTTTGAGGAC	CATGGCTTAC	CTTTCCTGCC	2400
TTTGACCCAT	CACACCCCAT	TTCTCTCTCT	TTCCCTCTCC	CCGCTGCCAA	TTCTGCAGC	2460
CCGGGGGAAC	CACTAGTT					2478

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 (2) INFORMATION FOR SEQ ID NO: 91:

30
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

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TCGGCCTTGC	TTTTGTGGYC	TTCTCTGTG	GCCAGAGCGT	TTTCATCACC	AAGCCTCCTG	60
ATGGCAGTNC	CTTCACCGAT	ATGTTCAAGA	TACTGACGTA	TTCTGCTGT	TCCCAGAAGC	120
GAAGTGGAGA	GCGCCAGAGT	AATGGTGAAG	GCAITGGAGT	NTTTCAGCAA	TCTTCTAAAC	180
AAAGTCTGTT	TGATTCATGT	AAGATGTCTC	ATGGTGGGCC	ATTTACAGAA	GAGAAAGTGG	240
AAGATGTGAA	AGCTCTGGTC	AAGATTGTCC	CTGTTTCTTT	GGCTTTGATA	CCTTACTGGA	300
CAGTGTATTT	CCAAATGCAG	ACAACATATG	TTTTACAGAG	TCTTCATTTG	AGGATTCCAG	360
AAATTTCAAA	TATTACAACC	ACTCCTCACA	CGCTCCCTGC	AGCCTGGCTG	ACCATGTTTG	420
ATGCTGTGCT	CATCCTCCTG	CTCATCCCTC	TGAAGGACAA	ACTGGTCGAT	CCCATTMTGA	480
GAAGACATGG	CCTGCTCCCA	TCCTCCCTGA	AGAGGATCGC	CGTGGGCATG	TTCTTTGTCA	540
TGTGCTCRGC	CTTTGCTGCA	GGAATTTTGG	AGAGTAAAAG	GCTGAACCTT	GTAAAGAGA	600
AAACCATTAA	TCAGACCATC	GGCAACGTCG	TCTACCATGC	TGCCGATCTG	TCGCTGTGGT	660
GGCAGGTGCC	GCAGTACTTG	CTGATTGGGA	TCAGCGAGAT	CTTTGCAAGT	ATCGCAGGCC	720
TGGAATTTGC	ATACTCAGCT	GCCCCCAAGT	CCATGCAGAG	TGCCATAATG	GGCTTGTCTT	780
TTTTCTTCTC	TGGCGTCGGG	TCGTTCTGTG	GTTCTGGACT	GCTGGCACTG	GTGTCTATCA	840

	AAGCCATCGG ATGGATGAGC AGTCACACAG ACTTTGGTAA TATTAACGGC TGCTATTTGA	900
5	ACTATTACTT TTTCCTTCTG GCTGCTATTC AAGGAGCTAC CCTCCTGCTT TTCCTCATTA	960
	TTTCTGTGAA ATATGACCAT CATCGAGACC ATCAGCGATC AAGAGCCAAT GGCGTGCCCA	1020
	CCAGCAGGAG GGCCTGACCT TCCTGAGGCC ATGTGCGGTT TCTGAGGCTG ACATGTCAGT	1080
10	AACTGACTGG GGTGCACTGA GAACAGGCAA GACTTTAAAT TCCCATAAAA TGTCTGACTT	1140
	CACTGAAACT TGCATGTTGC CTGGATTGAT TTCTTCTTTC CCTCTATCCA AAGGAGCTTG	1200
15	GTAAGTGCCT TACTGCAGCG TGTCTCCTGG CACGCTGGGC CCTCCGGGAG GAGAGCTGCA	1260
	GATTTTCGAGT ATGTCGCTTG TCATTCAAGG TCTCTGTGAA TCCTCTAGCT GGGTTCCCTT	1320
	TTTTACAGAA ACTCACAAAT GGAGATTGCA AAGTCTTGGG GAACTCCACG TGTAGTTGG	1380
20	CATCCCAGTT TCTTAAACAA ATAGTATCAC CTGCTTCCCA TAGCCATATC TCACTGTAAA	1440
	AAAAAAATT AATAAACTGT TACTTATATT TAAGAAAGTG AGGATTTTTT TTTTTTAAAG	1500
25	ATAAAAGCAT GGTGAGATGC TGCAAGGATT TTACATAAAT GCCATATTTA TGGTTTCCTT	1560
	CCTGAGAACA ATCTTGCTCT TGCCATGTTT TTTGATTTAG GCTGGTAGTA AACACATTTT	1620
	ATCTGCTGCT TCAAAAAGTA CTTACTTTTT AAACCATCAA CATTACTTTT CTTTCTTAAG	1680
30	GCAAGGCATG CATAAGAGTC ATTTGAGACC ATGTGTCCCA TCTCAAGCCA CAGAGCAACT	1740
	CACGGGGTAC TTCACACCTT ACCTAGTCAG AGTGCTTATA TATAGCTTTA TTTTGGTACG	1800
35	ATTGAGACTA AAGACTGATC ATGGTTGTAT GTAAGGAAAA CATTCTTTTG AACAGAAATA	1860
	GTGTAATTAA AAATAATTGA AAGTGTTAAA TGTGAACTTG AGCTGTTTGA CCAGTCACAT	1920
	TTTTGTATTG TTAAGTACG TGTATCTGGG GCTTCTCCGT TTGTTAATAC TTTTCTGTGA	1980
40	TTTGTGCTG TATTTTTGGC ATAACCTTAT TATAAAAAGC ATCTCAAATG CGAAWAAAA	2040
	AAAAAAAAA AAAAAAAC	2058

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(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 1411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

	GGCACAGGAG CGACCCGGA GAAGGAGGGC CAMGAKCGG AAGCGGAGGA GTCTCCAGGA	60
60	GACCCGGGGA CAGCATCGCC CAGGCCCTG TTTGCAGGCC TTTCAGATAT ATCCATCTCA	120

CAAGACATCC CCGTAGAAGG AGAAATCACC ATTCTATGA GATCTCGCAT CCGGGAGTTT 180
 GACAGCTCCA CATTAATGA ATCTGTTTCGC AATACCATCA TGCCTGATCT AAAAGCTGTT 240
 5 GGGAAAAAAT TCATGCATGT TTTGTACCCA AGGAAAAGTA ATACTCTTTT GAGAGATTGG 300
 GATTTGTGGG GCCCTTTGAT CCTTTGTGTG AACTTCGCAT TAATGCTGCA AAGAGACTCT 360
 GCAGATAGTG AAAAAGATGG AGGGCCCCAA TTTGCAGAGG TGTTTGTTCAT TGTCTGGTTT 420
 10 GGTGCAGTTA CCATCACCTT CAACTCAAAA CTTCTTGGAG GGAACATATC TTTTTCAG 480
 AGCCTCTGTG TGCTGGGTTA CTGTATACTT CCCTTGACAG TAGCAATGCT GATTTGCCGG 540
 CTGGTACTTT TGCTGATCC AGGACCTGTA AACTTCATGG TTCGGCTTTT TGTGGTGATT 600
 GTGATGTTTG CCTGGTCTAT AGTTGCCTCC ACAGCTTTCC TTGCTGATAG CCAGCCTCCA 660
 AACCGCAGAG CCTAGCTGT TTATCCTGTT TTCCTGTTTT ACTTTGTTCAT CAGTTGGATG 720
 20 ATTCTCACCT TTAATCCTCA GTAAATCAGG AATGGGAAAT TAAAAACCAG TGAATGAAA 780
 GCACATCTGA AAGATGCAAT TCACCATGGA GCTTTGTCTC TGGCCCTTAT TTGTCTAATT 840
 25 TTGGAGGTAT TTGATAACTG AGTAGGTGAG GAGATTAAAA GGGAGCCATA TAGCACTGTC 900
 ACCCCTTATT TGAGGAACTG ATGTTTGAAA GGCTGTCTCT TTCTCTCTTA ATGTCATTTT 960
 TTTAAAAATA CATGTGCATA CTACACACAG TATATAATGC CTCCTTAAGG CATGATGGAG 1020
 30 TCACCGTGGT CCATTTGGGT GACAACCAGT GACTTGGGAA GCACATAGAT ACATCTTACA 1080
 AGTTGAATAG AGTTGATAAC TATTTTCAGT TTTGAGAATA CCAGTTCAGG TGCAGCTCTT 1140
 35 AAACACATTG CCTTATGACT ATTAGAATAT GCCTCTCTTT TCATAAATAA AAATACATGG 1200
 TCTATATCCA TTTTCTTTTA TTTCTCTCTC TTAAGCTTAA AAAGGCAATG AGAGAGGTTA 1260
 GGAGTGGGTT CATAACGGA GAATGAGAAA ACATGCATTA ACCAATATTC AGATTTTGAT 1320
 40 CAGGGGAAAT TCTAYACTTG TTGCAAAAAA AAAAAAAAAA AACTTCGAGG GGGGCCCGGT 1380
 ACCCAATCGC NGTATATGAT CGNAAACAAT C 1411

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(2) INFORMATION FOR SEQ ID NO: 93:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GCTTTGGCTT TTTTGGCGG ACTGGGCGC CCTCCGGAAG CGTTTCCAAC TTTCCAGAAG 60
 60 TTTCTCGGA CGGCAGGAG GGGGTGGGA CTGCCATATA TAGATCCCGG GAGCAGGGGA 120

	GCGGGCTAAG	AGTAGAATCG	TGTCGCGCTC	GAGAGCGAGA	GTCACGTCCC	GGCGCTAGCC	180
	CAGCCCGACC	CAGGCCCACC	GTGGTGCACG	CAAACCACTT	CCTGGCCATG	CGCTCCCCTCC	240
5	TGCTTCTCAG	CGCCTTCTGC	CTCCTGGAGG	CGGCCCTGGC	CGCCGAGGTG	AAGAAACCTG	300
	CAGCCGCAGC	AGCTCCTGGC	ACTGCGGAGA	AGTTGAGCCC	CAAGGCGGCC	ACGCTTGCCG	360
10	AGCGCAGCCG	GCCTGGCCTT	CAGCTTGATC	CAGGCCATGG	CCAAGGACCA	GGCAGTGGAG	420
	AACATCCTGG	TGTCACCCGT	GGTGGTGGCC	TCGTCGCTGG	GGCTCGTGTC	GCTGGGCGGC	480
	AAGGCGACCA	CGGCGTCGCA	GGCCAAGGCA	GTGCTGAGCG	CCGAGCAGCT	GCGCGACGAG	540
15	GAGGTGCACG	CCGGCCTGGG	CGAGCTGCTG	CGCTCACTCA	GCAACTCCAC	GGCGCGCAAC	600
	GTGACCTGGA	AGCTGGGCAG	CCGACTGTAC	GGACCCAGCT	CAGTGAGCTT	CGCTGATGAC	660
20	TTCGTGCGCA	GCAGCAAGCA	GCACTACAAC	TGCGAGCACT	CCAAGATCAA	CTTCCGCGAC	720
	AAGCGCAGCG	CGCTGCAGTC	CATCAACGAG	TGGGCCGCGC	AGACCACCGA	CGGCAAGCTG	780
	CCCGAGGTCA	CCAAGGACGT	GGAGCGCACG	GACGGCGCCC	TGTTAGTCAA	CGCCATGTTT	840
25	TTCAAGCCAC	ACTGGGATGA	GAAATTCAC	CACAAGATGG	TGGACAACCG	TGGCTTCATG	900
	GTGACTCGGT	CCTATACCGT	GGGTGTCATG	ATGATGCACC	GGACAGGCCT	CTACAACCTAC	960
30	TACGACGACG	AGAAGGAAAA	GCTGCAAAATC	GTGGAGATGC	CCCTGGCCCA	CAAGCTCTCC	1020
	AGCCTCATCA	TCCTCATGCC	CCATCACGTG	GAGCCTCTCG	AGCGCCTTGA	AAAGCTGCTA	1080
	ACCAAAGAGC	AGCTGAAGAT	CTGGATGGGG	AAGATGCAGA	AGAAGGCTGT	TGCCATCTCC	1140
35	TTGCCCCAAGG	GTGTGGTGGG	GGTGACCCAT	GACCTGCAGA	AACACCTGGC	TGGGCTGGGC	1200
	CTGACTGAGG	CCATTGACAA	GAACAAGGCC	GACTTGTCAC	GCATGTCAGG	CAAGAAGGAC	1260
40	CTGTACCTGG	CCAGCGTGTT	CCACGCCACC	GCCTTTGAGT	TGGACACAGA	TGGCAACCCT	1320
	TTGACCAGAA	TTACGGGCGG	AGGAGTGCGC	ACCCAAGTGT	TCTACGCCGA	CCACCCCTTC	1380
	ATTTCCTAGT	GCGGGACACC	CAAAGCGGTC	CCTGCTATTG	ATTGGGCGCC	TGGTCCGGCC	1440
45	TAAGGGTGAC	AAGATGCGAG	ACGAGTTATA	GGCCTCAGGG	TGCACACAGG	ATGGCAGGAG	1500
	GCATCCAAAG	GCTCCTGAGA	CACATGGGTG	CTATTGGGGT	TGGGGGGGAG	GTGAGGTACC	1560
50	AGCCTTGAT	ACTCCATGGG	GTGGGGTGGG	AAAGCAGACC	GGGGTTCCCG	TGTGCCTGAG	1620
	CGGACTTCCC	AGCTAGAATT	CACTCCACTT	GGACATGGGC	CCCAGATACC	ATGATGCTGA	1680
	GCCCCGAAAC	TCCACATCCT	GTGGGACCTG	GGCCATAGTC	ATTCTGCCTG	CCCTGAAAGT	1740
55	CCCAGATCAA	GCCTGCCTCA	ATCAGTATTC	ATATTTATAG	CCAGGTACCT	TCTCACCTGT	1800
	GAGACCAAAT	TGAGCTAGGG	GGGTGAGCCA	GCCCTCTTCT	GACACTAAAA	CACCTCAGCT	1860
60	GCCTCCCCAG	CTCTATCCCA	ACCTCTCCCA	ACTATAAAAC	TAGGTGCTGC	AGCCCCCTGGG	1920

ACCAGGCACC CCCAGAATGA CCTGGCCGCA GTGAGGCGGA TTGAGAAGGA GCTCCCAGGA 1980
GGGGCTTCTG GGCAGACTCT GGTCAAGAAG CATCGTGTCT GCGTTGTGG GGATGAAC TT 2040
5 TTTGTTTTGT TTC TTCCTTT TTAGTTCTT CAAAGATAGG GAGGGAAGGG GGAACATGAG 2100
CCTTTGTTGC TATCAATCCA AGAACTTATT TGTACATTTT TTTTTTCAAT AAAACTTTTC 2160
10 CAATGACAAA AAAAAAAAAA AAAAAA 2187

15 (2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 757 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

25 GACAGTACGG TCGGATTCCC GGGTCGACCC ACGCGTCCGC GGACGGTGAA GAAGGTGAAG 60
ATGGCGGTGG CCAGGGCCGG GGTCTTGGGA GTCCAGTGGC TGCAAAGGGC ATCCCCGAAC 120
GTGATGCCGC TGGGCGCAGC GACAGCCTCC CACATGACCA AGGACATGTT CCCGGGGCCC 180
30 TATCCTAGGA CCCGAGAAGA ACGGGCCGCC GCCGCCAAGA AGTATAATAT GCGTGTGGAA 240
GACTACGAAC CTTACCCGGA TGATGGCATG GGGTATGGCG ACTACCCGAA GCTCCCTGAC 300
35 CGCTCACAGC ATGAGAGAGA TCCATGGTAT AGCTGGGACC AGCCGGGCCCT GAGGTTGAAC 360
TGGGGTGAAC CGATGCACTG GCACCTAGAC ATGTACAACA GGAACCGTGT GGATACATCC 420
CCCACACCTG TTTCTTGGCA TGTCTGTGT ATGCAGCTCT TCGGTTTCCT GGCTTTCATG 480
40 ATATTCATGT GCTGGGTGGG GGACGTGTAC CCTGTCTACC AGCCTGTGGG ACCAAAGCAG 540
TATCCTTACA ATAATCTGTA CCTGGAACGA GGCGGTGATC CCTCCAAAGA ACCAGAGCGG 600
45 GTGGTTCACT ATGAGATCTG AGGAGGCTTC GTGGGCTTTT GGGTCCTCTA ACTAGGACTC 660
CCTCATTCCT AGAAATTTAA CCTTAATGAA ATCCCTAATA AAACTCAGTG CTGTGTTAAA 720
50 AAAAAAAAAA AAAAAAAAAA AAAAAGGGGG GCCCCNN 757

55 (2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

5	GGCACGAGCA CTCCTGCACT TCCCCACCCC CACGACCGAA CCTGGCTTCG CTAACGCCCT	60
	CCCAGCTCCC TCGGCCTGA CTTCCGGTTT CTTCCGCGGT CCCTGGCGCC GAGCCGCGGA	120
	CAGCAGCCCC TTTTCCGGCT GAGAGCTCAT CCACACTTCC AATCACTTTC CGGAGTGCTT	180
10	CCCCCTCCCTC CGGCCCGTGC TGGTCCCGAC GGCGGGCCTG GGTCTCGCGC GCGTATTGCT	240
	GGGTAACGGG CCTTCTCYCG CGTCGGCCCG GCCCCTCCTG CCTCGGCTCG TCCCTCCTTC	300
	CAGAACGTCC CGGGCTCCTG CCGAGTCAGA AGAAATGGGA CTCCCTCCGC GACGTGCCCCG	360
15	GAGCAGCTCC CTTCTGCTGTG GAAGCGGCGG TGTCTTCGAA GAAACCGGAA GCCCGTGGTG	420
	ACCCCTGGCG ACCCGGTTTG TTTTCGGTCC GTTTCCAAAC ACTAAGGAAT CGAAACTCGG	480
20	CGGCCTTGGG GCGGCCCTA CGTAGCCTGG CTTCTGGTTG TCATGGATGC ACTGGTAGAA	540
	GATGATATCT GTATTCTGAA TCATGAAAAA GCCCATAAGA GAGATACAGT GACTCCAGTT	600
	TCAATATATT CAGGAGATGA ATCTGTTGCT TCCCATTTTG CTCTTGTCAC TGCATATGAA	660
25	GACATCAAAA AACGACTTAA GGATTGAGAG AAAGAGAACT CTTTGTATAA GAAGAGAATA	720
	AGATTTTTTG AAGAAAAGCT AATAGCTCGA TTTGAAGAAG AAACAAGTTC CGTGGGACGA	780
30	GAACAAGTAA ATAAGGCCTA TCATGCATAT CGAGAGGTTT GCATTGATAG AGATAATTTG	840
	AAGAGCAAAC TGGACAAAAT GAATAAAGAC AACTCTGAAT CTTTGAAAGT ATTGAATGAG	900
	CAGCTACAAT CTAAAGAAGT AGAACTCCTC CAGCTGAGGA CAGAGGTGGA AACTCAGCAG	960
35	GTGATGAGGA ATTTAAATCC ACCTTCATCA AACTGGGAGG TGGAAAAGTT GAGCTGTGAC	1020
	CTGAAGATCC ATGGTTTGGA ACAAGAGCTG GAACTGATGA GGAAAGAATG TAGCGATCTC	1080
40	AAAATAGAAC TACAGAAAGC CAAACAAACG GATCCATATC AGGAAGACAA TCTGAAGAGC	1140
	AGAGATCTCC AAAAATAAG CATTTCAAGT GATAATATGC AGCATGCATA CTGGGAAC TG	1200
	AAGAGAGAAA TGTCTAATTT ACATCTGGTG ACTCAAGTAC AAGCTGAACT ACTAAGAAAA	1260
45	CTGAAAACCT CAACTGCAAT CAAGAAAGCC TGTGCCCTTG TAGGATGCAG TGAAGACCTT	1320
	GGAAGAGACA GCACAAAAC GCACTTGATG AATTTTACTG CAACATACAC AAGACATCCC	1380
50	CCTCTCTTAC CAAATGGCAA AGCTCTTTGT CATAACACAT CTTCCCTTTT ACCAGGAGAT	1440
	GTAAAGGTTT TATCAGAGAA AGCAATCCTC CAATCATGGA CAGACAATGA GAGATCCATT	1500
	CCTAATGATG GTACATGCTT TCAGGAACAC AGTTCTTATG GCAGAAATTC TCTGGAAGAC	1560
55	AATTCCTGGG TATTTCCAAG TCCTCCTAAA TCAAGTGAGA CAGCATTTGG GGAACTAAA	1620
	ACTAAACTT TGCCTTACC CAACCTTCCA CCACTGCATT ACTTGATCA ACATAATCAG	1680
60	AACTGCCTTT ATAAGAATTA ATTTGGAAGA GATTACGAT TTCACCATGA GGACACTTAT	1740

5 CTCTTTCAGT GGTCTCCCA AGAAATTATT TAACAACTG AANGGAGATT TTGATTAAAA 1800
 TTTTGCAGAG GTCTTCAGTA TCTATATTTG AACACACTGT ACAATAGTAC AAAAACCAAC 1860
 ATAGTTGGTT TTCTAGTATG AAAGAGCACC CTCTAGCTCC ATATTCTAAG AATCTGAAAT 1920
 ATGCTACTAT ACTAATTAAT AAGTAACTT AAGGTGTTTA AAAAAGCTCTG CCTTCTATAT 1980
 10 TAATTGTAAA ATTTTGCCTC TCAGAAGAAT GGAATTGGAG ATTGTAGACG TGGTTTACAA 2040
 AAATGTGAAA TGTCTAAATA TCTGTTTATA AAAATAAAG GAAAACATGT TTCTTCAAAT 2100
 TGCATAATGG AACAAATGGC AATGTGAGTA GGTACATTT CTGTTGTTAT AATGCGTAAA 2160
 15 GATATTGAAA ATATAATGAA ATAAAAGCAT CTTAGGTTAT ACCATCTTTA TATGCTATTG 2220
 CGTTTCAATA TTTAAGATTT AAAGTGATTT TTTGGTCACA GTGTTTGTGTT GATAAAATTT 2280
 20 TTTTAGAATT GAAGTTTGAA TTCTAAGACT TGAAACAACC TGATCACTGA AGCCAACTTT 2340
 GTCCCAGCAC ATTCCTTAAG TCCTAATTGG GGAAAAAAA AAAAAAAAC TCGA 2394

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(2) INFORMATION FOR SEQ ID NO: 96:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

AGTGCTCTGT TGCCAGGCT GGAGTGCCTT AGTGTAATGT CAGTCCACTG CAACCTCCAC 60
 CCCCAGGTTT AAGCAATTCT CATGCCTCAG CCTCCAAGT AGCTGAAATT ACTGGCATGC 120
 40 ACCACCACAC CCAGCTGATG TTTATTTATT TATTTATATA TTTATTTATT TTAGGTGTTT 180
 TTTTTTTTTT TTTTGTGAGAC GGAGTCTTGC TCTGTTGCCC TGGGTGTGGT TACGTGGRAT 240
 45 TACCATYCTG GGTGACTCAC TGAAATGTAC TCMCAGTGAG TCATGCCTTC MAATGACATC 300
 TCAAGTTCTG CTGCTTGA GATACATCTG GGGATCTTAA GGGGTGAGGG ACTACTCAAC 360
 AAGAAGGAAT TTAGCCTGTC TTTTAAATA AACGGCATTT CTTTTTCCTA KAAAAATGGG 420
 50 AAATCTCTCA ATTCTCTAAT ACAGGGACAC TGAGATAACA AAGAGGAAAG TGTCTGGTTG 480
 GAGGTTGGGA RGCCACCCTG GGTCTCTCC TACAAAAATG GAAAAGAAA GAACGGTGAR 540
 55 AAATCMAGCA AAGCACAARA AAKTTTCCCT TTGCTAAAAG GGAAAAGATG CCCCMAATG 600
 CCCATAAACA TGAAGTGGG ATAAGGAGGA RAATGTCTCT YCTTGGCACC CCCAAACAAA 660
 CGTTAATTAC CC 672
 60

(2) INFORMATION FOR SEQ ID NO: 97:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1419 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

15 TAAGAACAGA ACAGCAAGTA TGAACCACAT GGAACCTAAA ACATATGGGT GTGAAGTCCA 60
 CTTATGTAGA CAAAACTTAT AATTTCCAAA CTGTTGTCTA GTATACAGTG ATCAGTTGCT 120
 CTCTGTTCAA GTCATTCCAC ACATTTCCCT ATTTTAGGCT ATTATAATAT AGAAAGAAAA 180
 20 TGGGAAGCAT TAGTTGGAGC TAGAAAATGA ACTGTATATT ATTGCTATAT TTGCTAATAC 240
 CAACTATTTT AATAAGTGT GTACCATATG TAGCATTAAA TATAAAATAC ATAAAAGAAT 300
 GTACAGAAAA TAGCTTTTAT TGAGTAATAT TACATTTTAT TTATACTGTA GCAATATATT 360
 25 TGTAGGTATA CTCTGTAAGG GCTTTAAATA AAAGAGGTCC ATTAATACTT CCTTATAAAA 420
 ATTCTAGTCT GTTTCATTAC TGCCCAGATG TTTTAGAGAT AAATATTTAT GCAGAAGGTA 480
 30 TTTTGGAAAG TCYCCYTTTG TCTGATAGAG TTTAACNAGA TATTTAAATT TAGTGCYCNA 540
 GAAATCCAC AAGTCACGGT CTAACACAC TTAGAATACT ACAGCATAAA TCTGTTAGCA 600
 TTANTTGCCA AATAAGACAG TTGGGATCCC AAACCCCAAG TCCTTGAGCA ATGTTTTTCC 660
 35 TCAAAAAGCT GCTATNCCAA TGATATAGGA AAACACATTG TGTTCCTTA AACACACTTT 720
 TCTTTTAAA TGTGCTTCAT TGTGTGATTT GGTCTGCCT AAATTCACA AGCTAGGCCA 780
 40 ATGAAGGCTG AATCAAAGAC ATTTTCATCCA CCAATATCAT GTGTAGATAT TATGTATAGA 840
 AAATAAAATA AATTATGGCT CTAACCTCTG TGTGCTGTT TATCTTGTTA TTTTTCGGCG 900
 TTATACTAAT GNGTTTATTG AGAGCATTTT ACCTTCAGA CTCTCATGG CTAACTTTGT 960
 45 GTCTGWATTT TGSTCCTTAG ATGKGAATAT TTCTTATTAG TYTGCTYCCT GCWACGCAAT 1020
 GACTGCATTT CTATCATTTT TCAGTTTGTT AGWATATGTG GATAGTATTC TACTGTATAA 1080
 50 ATGATTGCAA AGTTTATCAA AAACAAATTA TTATATGTAG CTTTCTACA GTGCTTTGCT 1140
 AAACCATGTA GTACTAGTTA AGTSTTCCTT GAAAATAAAG ATACACTCTT ATAGGGGACA 1200
 GTTCCTGTTT ACTCCCAGGA AACTTTTTTA AAAGATGACA CTGAATGTTT ATTGCACTTT 1260
 55 AGTGCAGTGA AGTGGCAATA AAACCTAACA TGAATCAAGG TTGTTTATGG CAGATGCATG 1320
 TGTGCTTTTA CAGAGTTTAG CAAAAGCTCT TAATTTTATG TCATACTGTA TTCTACTGAA 1380
 60 TAATAAAGCT AACATTATTC AATAATAAAA TGGAAAAA 1419

5 (2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

15 GCGACCGCGC CCCTTTCAGC TAGCTCGCTC GCTCGCTCTG CTTCCCTGCT GCCGGCTGCG 60
 CATGGCKWTG GCGTTGGCGG CGCTGGCGGC GGTGAGCCG GCCTGCGCAG CCGGTACCAG 120
 CAGTTGCAGA ATGAAGAAGA GTCTGGAGAA CCTGAACAGG CTGCAGGTGA TGCTCCTCCA 180
 20 CCTTACAGCA GCATTTCTGC AGAGAGCGCA GTTTTCCACC TATTTCCCTG GATATTTTGA 240
 TGGTCAGTAC TGGCTCTGGT GGGTGTTCCT TGTMTTAGGC TTTCTCCTGT TTCTCAGAGG 300
 25 ATTTATCAAT TATGCAAAAG TTCGGAAGAT GCCAGAACT TTCTCAAATC TCCCCAGGAC 360
 CAGAGTTCTC TTTATTTATT AAAGATGTTT TCTGGCAAAG GCCTTCCTGC ATTTATGAAT 420
 TCTCTCTCAA GAAGCAAGAG AACACCTGCA GGAAGTGAAT CAAGATGCAG AACACAGAGG 480
 30 AATAATCACC TGCTTTAAAA AAATAAAGTA CTGTTGAAAA GATCATTTCT CTCTATTTGT 540
 TCCTAGGTGT AAAATTTTAA TAGTTAATGC AGAATTCTGT AATCATTGAA TCATTAGTGG 600
 35 TTAATGTTTG AAAAAGCTCT TGCAATCAAG TCTGTGATGT ATTAATAATG CCTTATATAT 660
 TGTTTGTAGT CATTTTAAGT AGCATGAGCC ATGTCCCTGT AGTCGGTAGG GGGCAGTCTT 720
 GCTTTATPCA TCCTCCATCT CAAAATGAAC TTGGAATTAA ATATTGTAAG ATATGTATAA 780
 40 TGCTGGCCAT TTTAAAGGGG TTTTCTCAA AGTTAAACTT TTGTTATGAC TGTGTTTTTG 840
 CACATAATCC ATATTTGCTG TTCAAGTTAA TCTAGAAATT TATTCAATTC TGTATGAACA 900
 45 CCTGGAAGCA AAATCATAGT GCAAAAATAC ATTTAAGGTG TGGTCAAAAA TAAGTCTTTA 960
 ATTGGTAAAT AATAAGCATT AATTTTTTAT AGCCTGTATT CACAATTCTG CGGTACCTTA 1020
 TTGTACCTAA GGGATTCTAA AGGTGTTGTC ACTGTATAAA ACAGAAAGCA CTAGGATACA 1080
 50 AATGAAGCTT AATTACTAAA ATGTAATTCT TGACACTCTT TCTATAATTA GCGTTCTTCA 1140
 CCCCCACCCC CACCCCCACC CCCCTTATTT TCCTTTTGTC TCCTGGTGAT TAGGCCAAAG 1200
 55 TCTGGGAGTA AGGAGAGGAT TAGGTACTTA GGAGCAAAGA AAGAAGTAGC TTGGAACCTT 1260
 TGAGATGATC CCTAACATAC TGTAATACTT GCTTTTACAA TGTGTTAGCA GAAACCAAGT 1320
 60 GGTATAATG TAGAATGATG TGCTTTCTGC CCAAGTGGTA ATTCATCTTG GTTTGCTATG 1380

TTAAAACTGT AAATACAACA GAACATTAAT AAATATCTCT TGTGTAGCAC CTTTAAAAAA 1440
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAN CCCGGGGGGG GGCCCCN 1487

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(2) INFORMATION FOR SEQ ID NO: 99:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1653 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

GCGACCGCGC CCTTCAGCTA GCTCGCTCGC TCGCTCTGCT TCCCTGCTGC CGGCTGCGCA 60
 20 TGGCTTNGGC GTTGGCGGCG CTGGCGGCGG CTCGAGCCGC CTGCGSAGCC GGTACCAGCA 120
 GTTGCAGAAT GAAGAAGAGT CTGAGAACC TGAACAGGCT GCAGGTGATG CTCCTCCACC 180
 25 TTACAGCAGC ATTTCTGCAG AGAGCGCACA TNATTTTGAC TACAAGGATG AGTCTGGGTT 240
 TCCAAAGCCC CCATCTTACA ATGTAGCTAC AACACTGCCC AGTTATGATG AAGCGGAGAG 300
 GACCAAGGCT GAAGCTACTA TCCCTTTGGT TCCTGGGAGA GATGAGGATT TTGTGGGTCG 360
 30 GGATGATTTT GATGATGCTG ACCAGCTGAG GATAGGAAAT GATGGGATTT TCATGTTAAC 420
 TTTTTCATG GCATTCTCT TTAAGTGGAT TGGGTTTTTC CTGTCTTTT GCCTGACCAC 480
 TTCAGCTGCA GGAAGGTATG GGGCCATTTC AGGATTTGGT CTCTCTCTAA TTAAATGGAT 540
 35 CCTGATGTC AGGTTTTCCA CCTATTTCCC TGCATTTATG AATTCTCTCT CAAGAAGCAA 600
 GAGAACACCT GCAGGAAGTG AATCAAGATG CAGAACACAG AGGAATAATC ACCTGCTTTA 660
 40 AAAAAATAAA GTACTGTTGA AAAGATCATT TCTCTCTATT TGTTCCTAGG TGTAATAATT 720
 TAATAGTTAA TGCAGAATTC TGTAATCATT GAATCATTAG TGGTTAATGT TTGAAAAAGC 780
 TCTTGCAATC AAGTCTGTGA TGTATTAATA ATGCCTTATA TATTGTTTGT AGTCATTTTA 840
 45 AGTAGCATGA GCCATGTCCC TGTAGTCGGT AGGGGGCAGT CTGCTTTTAT TCATCCTCCA 900
 TCTCAAAATG AACTTGGAAT TAAATATTGT AAGATATGTA TAATGCTGGC CATTTTAAAG 960
 50 GGGTTTCTC AAAAGTTAAA CTTTGTATAT GACTGTGTTT TTGCACATAA TCCATATTTG 1020
 CTGTTCAAGT TAATCTAGAA ATTTATTCAA TTCTGTATGA ACACCTGGAA GCAAAATCAT 1080
 AGTGCAAAAA TACATTTAAG GTGTGGTCAA AAATAAGTCT TTAATTGGTA AATAATAAGC 1140
 55 ATTAATTTTT TATAGCCTGT ATTCACAATT CTGCGGTACC TTATTGTACC TAAGGGATTC 1200
 TAAAGGTGTT GTCACGTAT AAAACAGAAA GCACTAGGAT ACAAATGAAG CTTAATTACT 1260
 60 AAAATGTAAT TCTTGACACT CTTTCTATAA TTAGCGTTCT TCACCCCCAC CCCCACCCCC 1320

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ACCCCCCTTA TTTTCCTTTT GTCTCCTGGT GATTAGGCCA AAGTCTGGGA GTAAGGAGAG 1380
 GATTAGGTAC TTAGGAGCAA AGAAAGAAGT AGCTTGGAAC TTTTGAGATG ATCCCTAACA 1440
 TACTGTACTA CTTGCTTTTA CAATGTGTTA GCAGAAACCA GTGGGTTATA ATGTAGAATG 1500
 ATGTGCTTTC TGCCCAAGTG GTAATTCATC TTGGTTTGCT ATGTTAAAAC TGTAAATACA 1560
 ACAGAACATT AATAAATATC TCTTGTGTAG CACCTTTTAW AAAAAAAAAA AAAAAAAAAA 1620
 AAAAAAAAAA AAAAANCCCG GGGGGGGGCC CCN 1653

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

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TTTTMTTTT TTTTMTTTT TTGACTGAAC TAAGTGGCTT TTTTATTAGA GAAAGCCAGA 60
 ATTACAAAAG ACTTCCCTTT TCTTGGGGTA TGGCTGTCTC AGCACAATAC TCAACATAAC 120
 TGCAGAACTG ATGTGGCTCA GGCACCCTGG TTTTAATPCC TTGAGGATCT GGCAATTGGC 180
 TTACGCAAAA GGTCAACCAT TGAGGTCCTG CCTTACTAAT TATGTGCTGC CCAACAACCTA 240
 AATTGTGAAT TTGTTTTTCT CTAGTTTGAG CAGGGTCTGA ATTTTTTCAT TTATTTCTTT 300
 TTTTGCCAGC AGACAGACTT GAGTCTGTAA AGACAAGCAA ATACACTGAC AGAAGTTTAC 360
 CATAGTTTCT AAAATGTAAA AAAGAAAACC CCCAAAAGAC TCAAGAAAAT TAGACCACAA 420
 ATTTTGCATT GTTCATTGTA GCACTATTGG TAATAAATA ACAAATGTTT GTGCATTTTT 480
 ATGTGAAGAT CCTTCTCGTA TTTCATTGG AAAGATGAGC AAGAGGTCTG CTTCCCTTCAT 540
 TTTACTTCCC CTCTGTTTTT TGAAAGGCAG TTTCGCCAAG CTTAATGCAA GAATATCTGA 600
 CTGTTTAGAA GAAAGATATT GCCACAATCT CTGGATGGTT TTCCAGGGTT GTGTTATTAC 660
 TGAGCTTCAT CTTTCCAGAA TGAGCAAAAC ACTGTCCAGT CTTTGTACG ATTTTGTAAT 720
 AAATGTGTAC ATTTTMTTTA AATTTTGGGA CATCATGA ATAAAGGTAT GTATGTACGA 780
 ATGTGTATAT ATTATATATA TGACATCTAT TTTGGAAAAT GTTTGCCCTG CTGTACCTCA 840
 TTTTATAGGAG GTGTGCATGG ATGCAATATA TGAAAATGGG ACATTCTGGA ACTGCTGGTC 900
 AGGGGACTTT GTCGCCCTGT GCACTAAAAG GGCCAGATTT TCAGCAGCCA AGGACATCCA 960
 TACCCAAGTG AATGTGATGG GACTTAAAAG AAGTGAAGT AGACAATTCA CTCTGGCTGT 1020

TTGAACAGCA GCGTTTCATA GGAAGAGAAA AAAAGATCAA TCTTGTATTT TCTGACCACA 1080
TAAAGGCTTC TTCTCTTTGT AATAAAGTAG AAAAGCTCTC CTCAAAAAAA AAAAAAAAAA 1140
5 AAAAA 1145

10 (2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 734 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

20 TACCCGCGCGG ATTCAGGAA GGTAATTTA GTCCTATAAT TTTCAGCTTA ATTATAAACA 60
AAGGAACAAA TAAGTGAAG GGCAGCTATT ACCATTCGCT TAGTCAAAAC ATTCGGTTAC 120
25 TGCCCTTTAA TACACTCCTA TCATCAGCAC TTCCACCATG TATTACAAGT CTTGACCCAT 180
CCCTGTCGTA ACTCCAGTAA AAGTTACTGT TACTAGAAAA TTTTATCAA TTAAGTGACA 240
AATAGTTTCT TTTTAAAGTA GTTCTTCCA TCTTTATTCT GACTAGCTTC CAAAATGTGT 300
30 TCCCTTTTGG AATCGAGGTT TTTTGTGTTT GTTTGTGTTT CTGAAAAAAT CATACAACCT 360
TGTGCTTCTA TTGCTTTTTT GTGTTTGTGTT AAGCATGTCC CTTGGCCCAA ATGGAAGAGG 420
AAATGTTTAA TTAATGCTTT TTAGTTTAAA TAAATGAAT CATTTATAAT AATCAGTGTT 480
35 AACAAATTAG TGACCCCTGG TAGGTTAAAG GTTGCATTAT TTATACTTGA GATTTTTTTC 540
CCCTAACTAT TCTGTTTTTT GTACTTTAAA ACTATGGGGG AAATATCACT GGTCTGTCAA 600
40 GAAACAGCAG TAATTATTAC TGAGTTAAAT TGAAAAGTCC AGTGGACCAG GCATTTCTTA 660
TATAAATAAA ATTGGTGGTA CTAATGTGAA AAAAAAAAAA AAAAAAACT CGAGGGGGGC 720
45 CCGGTACCCT ATTA 734

50 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

60 CCGCGGGAAC GCTGTCCTGG CTGCCGNCAC CCGAACAGCC TGTCTTGGTG CCGCGGCTCC 60

CTGCCCCGCG CCCAGTCATG ACCCTGCGCC CCTCACTCCT CCCGCTCCAT CTGCTGCTGC 120
 TGCTGCTGCT CAGTGCGGCG GTGTGCCGGG CTGAGGCTGG GCTCGAAACC GAAAGTCCCCG 180
 5 TCCGGACCCT CCAAGTGGAG ACCCTGGTGG AGCCCCCAGA ACCATGTGCC GAGCCCGCTG 240
 CTTTGGAGA CACGCTTCAC ATACACTACA CGGGAAGCTT GGTAGATGGA CGTATTATTG 300
 ACACCTCCCT GACCAGAGAC CCTCTGGTTA TAGAACTTGG CCAAAGCAG GTGATTCCAG 360
 10 GTCTGGAGCA GAGTCTTCTC GACATGTGTG TGGGAGAGAA GCGAAGGGCA ATCATTCCTT 420
 CTCACCTGGC CTATGGAAAA CGGGGATTTT CACCATCTGT CCCAGCGGAT GCAGTGGTGC 480
 15 AGTATGACGT GGAGCTGATT GACTAATCC GAGCCAAC TA CTGGCTAAAG CTGGTGAAGG 540
 GCATTTTGCC TCTGGTAGGG ATGGCCATGG TGCCACCCTC CTGGGCCTCA TTGGGTATCA 600
 CCTATACAGA AAGGCCAATA GACCCAAAGT CTCCAAAAAG AAGCTCAAGG AAGAGAAACG 660
 20 AAACAAGAGC AAAAAGAAAT AATAAATAAT AAATTTTAAA AAACCTAAAA AAA 713

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(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

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CCGATGTGGA CATCATCCTG TCTATCCCCA TGTTCCTGCG CCTGTACCTG ATCGCCCGAG 60
 TCATGCTGCT GCACAGAAGC TCTTCACCGA TGCCTCGTCC CGCAGCATCG GGGCCCTCAA 120
 40 CAAGATCAAC TTCAACACCC GCTTTGTCAT GAAGACGCTC ATGACCATCT GCCCTGGCAC 180
 TGTGCTGCTC GTGTTAGCA TCTCTCTGTG GATCATGTCT GCCTGGACCG TCCGTGTCTG 240
 TGAAAGTCCT GAATCACCAG CCCAGCCTTC TGGCTCATCA CTTCTCTGCTT GGTACCATGA 300
 45 CCAGCAGGAC GTAAC TAGTA ACTTTCTGGG TGCCATGTGG CTCATCTCCA TCACATTCCT 360
 TTCCATTGGT TATGGGGACA TGGTGCCCCA CACATACTGT GGGAAAGGTG TCTGTCTCCT 420
 50 CACTGGCATC ATGGGTGCAG GCTGCACTGC CCTTGTGGTG GCCGTGGTGG CCCGAAAGCT 480
 GGAAC TACC AAAGCGGAGA AGCACGTTCA TAANTTCATG ATGGACACTC AGCTACCAA 540
 GCGGATCAAG AATGYTGAG CCAATGTCCT TSGGGAAACA TGGTTAATCT ATAAACACAC 600
 55 AAAGYTGYTA AAGAAGATTG ACCATGCCAA AGTGAGGAAC ACCAGAGGAA GTTCYTCCAA 660
 GTATCCACCA GTTGAGGAGC GTCAAGATGG AACAGAGGAA GCTGAGTGAC CAAGCCAACA 720
 60 NICTGGTGA CCTTTCCAAG ATGCAGAATG TCMTGTATGA CTTAATCACA GAACTCAATG 780

ACCGGAGCGA AGACCTGGAG AAGCAGATTG GCAGCCTGGA GTCGAAGCTG GAGCATCTCA 840
CCGCCAGCTT CAACTCCCTG CCGCTGCTCA TCGCCGACAC CCTGCGCCAG CAGCAGCAGC 900
5 AGCTCCTGTC TGCCATCATC GAGGCCCGGG GTGTCAGCGT GGCAGTGGGC ACCACCCACA 960
CCCCAATCTC CGATAGCCCC ATTGGGGTCA GCTCCACCTC CTTCCCGACC CCGTACACAA 1020
10 GTTCAAGCAG TTGCTAAATA AATCTCCCCA CTCCAGAAGC ATTAAAAAAA AAAAAAAAAA 1080

15 (2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

25 GGCACGAGAG GCTTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT CACCACCATG 60
AAGTTCCTAG CAGTCCTGGT ACTCTTGGGA GTTTCATCT TTCTGGTCTC TGCCAGAAT 120
CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGCTGA TGATGAAGCC 180
30 CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC TACCACTGCA 240
ACCACCGCTG CTTCTACCAC TGCTCGTAAA GACATTCCAG TTTTACCCAA ATGGGTGGG 300
35 GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT TCTGCAATTG 360
GTCACAAC TAATCATGCTTC CTGTGATTTC ATCCAAC TACCTTGCC TACGATATCC 420
CCTTTATCTC TAATCAGTTT ATTTCTTTT AAATAAAAAA TAACTATGAG CAACAAAAA 480
40 AAAAAAAA 489

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(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

55 GCGGTCGCGG CTGTTGTGTG GTCCCCATG GAGCTGCCGT AGCGGACCCA GCACAGCCAG 60
GAGCGTCCGG GATGAGCTCA GCCGCGCCG ACCACTGGGC GTGGTTGCTG GTGCTCAGCT 120
60 TCGTGTTGG ATGCAATGTT CTTAGGATCC TCCTCCCGTC CTTCTCATCC TTCATGTCCA 180

5 GGGTGCTGCA GAAGGACGCG GAGCAGGAGT CACAGATGAG AGCGGAGATC CAGGACATGA 240
 AGCAGGAGCT CTCCACAGTC AACATGATGG ACGAGTTTGC CAGATATGCC AGGCTGGAAA 300
 GAAAGATCAA CAAGATGACG GATAAGCTCA AAACCCATGT GAAAGCTCGG ACAGCTCAAT 360
 TAGCCAAGAT AAAATGGGTG ATAAGTGTCTG CTTTCTACGT ATTGCAGGCT GCCCTGATGA 420
 10 TCTCACTCAT TTGGAAGTAT TATTCTGTCC CTGTGGCTGT CGTGCCGAGT AAATGGATAA 480
 CCCTYTAGAC CGCCTGGTAG CCTTTCCYAY TAGAGTAGCA GGTGGTGTG GAATTACTGT 540
 TGGATTTART CTGTACAAAT TGTCCATTG TGCTTCACCG TYCASTGAAC AGGAGGTGGT 600
 15 ACAGCCGGAG TTAAAAACGG TTTCCNTTCC AGTTTAAAT 640

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(2) INFORMATION FOR SEQ ID NO: 106:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1529 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

30 GGGCACNAGA TGGAGCTGCC GTAGCGGACC CAGCACAGCC AGGAGCGTCC GGGATGAGCT 60
 CAGCCGCGGC CGACCACTGG GCGTGGTTGC TGGTGCTCAG CTTCTGTGTT GGATGCAATG 120
 35 TTCTTAGGAT CCTCCTCCCG TCCTTCTCAT CCTTCATGTC CAGGGTGCTG CAGAAGGACG 180
 CGGACAGGAG TCACAGATGA GAGCGGAGAT CCAGGACATG AAGCAGGAGC TCTCCACAGT 240
 CAACATGATG GACGAGTTTG CCAGATATGC CAGGCTGGAA AGAAAGATCA ACAAGATGAC 300
 40 GGATAAGCTC AAAACCCATG TGAAAGCTCG GACAGCTCAA TTAGCCAAGA TAAATGGGT 360
 GATAAGTGTC GCTTTCTACG TATTGCAGGC TGCCCTGATG ATCTCACTCA TTTGGAAGTA 420
 45 TTATTCTGTC CCTGTGGCTG TCGTGCCGAG TAAATGGATA ACCCCTCTAG ACCGCCTGGT 480
 AGCCTTTCTT ACTAGAGTAG CAGGTGGTGT TGGAATTACC TGTGGATTT TAGTCTGTAA 540
 CAAAGTTGTC GCTATTGTGC TTATCCGTT CAGCTGAACA GGAGGATGGA TACAGCCGCG 600
 50 AGTAAAAAAA CGGATTTCTT CTTCCTAGCT TAAAATCTGA TTTACACTGT TTTGTTTTTT 660
 AAGAAACAAA AGTGCATAGT TTAGATTTTT TTTTGTGTA ATATGTTTGT TCTTGGACTT 720
 55 TATGAGATAG TCTTATAAGA ATCAGATTT TCTACACCTG TCATTGAGCC AAGAAAGTCC 780
 AGTTTATGAC ACGTATGTAC TAGTGAACAC CGTCCTCGAT CTGTACGAAA TGTGAAATGT 840
 TTAGGGACAT CTCATGCTG TCACTGTGA TTTGCCCTCT TATGTATTTT GGTCAATTTG 900
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	CCAACTGGAA AGTCAAAATT TTCTAACAAC TTTAAGTAAG TTCITTGAAG ACTTAGTGCT	960
	GTTTTTAATC CAGTTTAGAA AGTAACTTAA TTTTAATACC RCTACTAAAA ATTGCGAAAT	1020
5	TTCTTCTTTA ATCACATTCA ATATGGTTAA AAGAACAACA CTAATTGACA TTGCGTGGGC	1080
	TTTTTCTCCC TTGTGTTAAA ATGTCATTG TTGAGCAAGA GTTGTATAGT ATTATCTACT	1140
10	TACTTGAGGC TGTTAATTTT TCATTACAGT GTTTTGTAAG TGTATCCACG AGACCATGAT	1200
	GCATTGTTTT GTGCTCAACT TGTGTTTTGT ATTTAAAGCA TTTTGAATGA AGTGTATTTT	1260
	ATAAGCATTT AATATTTATG CTCTTTAGAA TGGAACACAG AAAACAAACC TTATAAGTCC	1320
15	TGATTAATCT GAACCAATAA CCTGTGTGGC CTACAAAGTA TAATTCATT AAATGTTTCT	1380
	TAAACACTT TTTTCTAATT AAAATCTTTG CAAATGCTTG TGTAACCTCC TGCCTTACAG	1440
20	CTACTGTTT GCTGTGAGCC ACCCGCAACT GACAAGTGGC TGTTAAGTGA GTCACCATAT	1500
	CCCAGTAAAG CTGAATTTTC TCACTAAAA	1529

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(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

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	ATGAAGGGTC GTTGGTGGA AAGATGGCGG CGACTCTGGG ACCCCTTGGT CGTGGCAGCA	60
	GTGGCGRCGA TGTTGTGCG CTCGGGATGG GTCCAGGATG TTACTCCTTC TTCTTTTGTT	120
40	GGGGTCTGGG CAGGGGCCAC AGCAAGTCGG GCGGGTCAA ACGTTCGAGT ACTTGAAACG	180
	GGAGCACTCG CTGTCGAAGC CCTACCAGG TGTGGGCACA GGCAGTTCCT CACTGTGGAA	240
45	TCTGATGGGC AATGCCATGG TGATGACCCA GTATATCCGC CTTACCCAG ATATGCAAAG	300
	TAAACAGGGT GCCTTGTGGA ACCGGGTGCC ATGTTTCCTG AGAGACTGGG AGTTGCAGGT	360
	GCACCTCAAA ATCCATGGAC AAGGAAAGAA GAATCTGCA TGGGATGGCT TGGCAATCTG	420
50	GTACACAAAG GRWTCGGATG CAGCCAGGGC CTGTNTTTGG GAAACATGGA CAAATTTGTG	480
	GGGCTGGGAG TATTGTAGA CACCTACCCC AATGAGGAGA AGCAGCAAGA GCGGGTATTC	540
55	CCCTRCMTCT CAGCCATGGT GAACAACGGC TCCCTCAGCT ATGATCATGA GCGGGATGGG	600
	CGGCCTACAG AGCTGGGAGG CTGCASAGCC ATTGTCCGCA ATCTTCATTA CGACACCTTC	660
	CTGGTGATTC GCTACGTCAA GAGGCATTTR ACGATAATGA TGGATATTGA TGGCAAGCAT	720
60	GAGTGGAGGG ACTGCATTGA AGTGCCCGGA GTCCGCCTGC CCCGCGGCTA CTACTTCGGC	780

	ACCTCCTCCA TCACTGGGGA TCTCTCAGAT AATCATGATG TCATTTCTCTT GAAGTTGTTT	840
	GAAGTGACAG TGGAGAGAAC CCCAGAAGAG GAAAAGCTCC ATCGAGATGT GTTCTTGCCC	900
5	TCAGTGGACA ATATGAAGCT GCCTGAGATG ACAGCTCCAC TGCCGCCCCCT GAGTGGCCTG	960
	GGCCTCTTCC TCATCGTCTT TTTCTCCCTG GGTGTTTTCT GTATTTGCCA TAGTCATTGG	1020
10	TATCATACTC TACAACAAAT GGCAGGAACA GAGCCGAAAG CGCTTCTACT GAGCCCTCCT	1080
	GCTGCCACCA CTTTTGTGAC TGTCACCCAT GAGGTATGGA AGGAGCAGGC ACTGGCCTGA	1140
	GCATGCAGCC TGGAGAGTGT TCTTGTCTCT AGCAGCTGGT TGGGGACTAT ATTCTGTCAC	1200
15	TGGAGTTTTG AATGCAGGGA CCCCGCATTC CCATGGTTGT GCATGGGGAC ATCTAACTCT	1260
	GGTCTGGGAA GCCACCCACC CCAGGGCAAT GCTGCTGTGA TGTGCCTTTC CCTGCAGTCC	1320
20	TTCCATGTGG GAGCAGAGGT GTGAAGAGAA TTTACGTGGT TGTGATGCCA AAATCACAGA	1380
	ACAGAAATTC ATAGCCCAGG CTGCCGTGTT GTTTGACTCA GAAGGCCCTT CTACTTCAGT	1440
	TTTGAATCCA CAAAGAATTA AAAACTGGTA ACACCACAGG CTTTCTGACC ATCCATTCGT	1500
25	TGGGTTTTGC ATTTGACCCA ACCCTCTGCC TACCTGAGGA GCTTTCTTTG GAAACCAGGA	1560
	TGGAAACTTC TTCCCTGCCT TACCTTCCTT TCACTCCAAT CATTGTCCTC TCTGTGTGCA	1620
30	ACCTGAGCTG GGAAAGGCAT TTGGATGCCT CTCTGTTGGG GCCTGGGGCT GCAGAACACA	1680
	CCTGCGTTTC ACTGGCCTTC ATTAGGTGGC CCTAGGGAGA TGGCTTTCTG CTTTGGATCA	1740
	CTGTTCCTTA GCATGGGTCT TGGGTCTATT GGCATGTCCA TGGCCTTCCC AATCAAGTCT	1800
35	CTTCAGGCCC TCAGTGAAGT TTGGCTAAAG GTTGGTGTAA AAATCAAGAG AAGCCTGGAA	1860
	GACATCATGG ATGCCATGGA TTAGCTGTGC AACTGACCAG CTCCAGGTTT GATCAAACCA	1920
40	AAAGCAACAT TTGTCATGTG GTCTGACCAT GTGGAGATGT TTCTGGACTT GCTAGAGCCT	1980
	GCTTAGCTGC ATGTTTTGTA GTTACGATTT TTGGAATCCC ACTTTGAGTG CTGAAAGTGT	2040
	AAGGAAGCTT TCTTCTTACA CCTTGGGCTT GGATATTGCC CAGAGAAGAA ATTTGGCTTT	2100
45	TTTTTTNCTT AATGGACAAG AGACAGTTGC TGTCTCATG TTCCAAGTCT GAGAGCAACA	2160
	GACCCTCATC ATCTGTGCCT GGAAGAGTTC ACTGTCATTG AGCAGCACAG CCTGAGTGCT	2220
50	GGCCTCTGTC AACCCTTATT CCACTGCCTT ATTTGACAAG GGGTTACATG CTGCTCACCT	2280
	TACTGCCCTG GGATTAAATC AGTTACAGGC CAGAGTCTCC TTGGAGGGCC TGGAACCTG	2340
	AGTCCTCCTA TGAACCTCTG TAGCCTAAAT GAAATTCCTA AAATCACCGA TGGAACCAAA	2400
55	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAN	2435
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(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 805 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

10 ATGAAACTTA AGAATTGAAT TGGAAAGACT TCTCAAAGAG AATTGTATGT AACGATGTTG 60
TATTGATTTT TAAGAAAGTA ATTTAATTTG TAAACTTCT GCTCGTTTAC ACTGCACATT 120
15 GAATACAGGT AACTAATTGG AAGGAGAGGG GAGGTCACCTC TTTTGATGGT GGCCCTGAAC 180
CTCATTCTGG TTCCCTGCTG CGCTGCTTGG TGTGACCCAC GGAGGATCCA CTCCCAGGAT 240
GACGTGCTCC GTAGCTCTGC TGCTGATACT GGGTCTGCGA TGCAGCGGCG TGAGGCCTGG 300
20 GCTGGTTGGA GAAGGTCACA ACCCTTCTCT GTTGGTCTGC CTTCTGCTGA AAGACTCGAG 360
AACCAACCAG GGAAGCTGTC CTGGAGGTCC CTGGTCGGAG AGGGACATAG AATCTGTGAC 420
25 CTCTGACAAC TGTGAAGCCA CCCTGGGCTA CAGAAACCAC AGTCTTCCCA GCAATTATTA 480
CAATTCTTGA ATTCCTTGGG GATTTTTTAC TGCCCTTTCA AAGCACTTAA GTGTTAGATC 540
TAACGTGTTC CAGTGTCTGT CTGAGGTGAC TTAAAAATC AGAACAAAAC TTCTATTATC 600
30 CAGAGTCATG GGAGAGTACA CCCTTCCAG GAATAATGTT TTGGGAAACA CTGAAATGAA 660
ATCTTCCAG TATTATAAAT TGTGTATTTA AAAAAAGAA ACTTTTCTGA ATGCCTACTG 720
35 GCGGTGTATA CCAGGCAGTG TGCCAGTTTA AAAAGATGAA AAAGAATAAA AACTTTTGAG 780
GAACAAAAAA AAAAAAAAAA AAATT 805

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(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGCACGAGAG GCGCCAGTCG CAGGTGTGCT GCTGAGGCGT GAGAATGGCG TCCCGCGGCC 60
GGCGTCCGGA GCATGGCGGA CCCCAGAGC TGTTTTATGA CGAGACAGAA GCCCGGAAAT 120
55 ACGTTCGCAA CTCACGGATG ATTGATATCC AGACCAGGAT GGCTGGGCGA GCATTGGAGC 180
TTCTTTATCT GCCAGAGAAT AAGCCCTGTT ACCTGCTGGA TATTGGCTGT GGCCTGGGC 240
60 TGAGTGGAAG TTATCTGTCA GATGAAGGGC ACTATTGGGT GGCCTGGAT ATCAGCCCTG 300

CCATGCTGGA TGAGGCTGTG GACCGAGAGA TAGAGGGAGA CCTGCTGCTG GGGGATATGG 360
 GCCAGGGCAT CCCATTCAAG CCAGGCACAT TTGATGGTTG CATCAGCAIT TCTGCTGTGC 420
 5 AGTGGCTCTG TAATGCTAAC AAGAAGTCTG AAAACCCTGC CAAGCGCCTG TACTGCTTTT 480
 TTGCTTCTCT TTTTCTGTGTT CTCGTCCGGG GATCCCAGAGC TGTCTGCAG CTGTACCCTG 540
 10 AGAACTCAGA GCAGTTGGAG CTGATCACAA CCCAGGCCAC AAAGGCAGGC TTCTCCGGTG 600
 GCATGGTGGT AGACTACCCT AACAGTGCCA AAGCAAAGAA ATTCTACCTC TGCTTGTTTT 660
 CTGGGCCTTC GACCTTTATA CCAGAGGGGC TGAGTGAAAA TCAGGATGAA GTTGAACCCA 720
 15 GGGAGTCTGT GTTCACCAAT GAGAGGTTCC CATTAAAGAT GTCGAGGCGG GGAATGGTGA 780
 GGAAGAGTCG GGCATGGGTG CTGGAGAAGA AGGAGCGGCA CAGGCGCCAG GGCAGGGAAG 840
 20 TCAGACCTGA CACCCAGTAC ACCGGCCGCA AGCGCAAGCC CCGCTTCTAA GTCACCACGC 900
 GGTCTGGAA AGGCACTTGC CTCTGCACTT TTCTATATTG TTCAGCTGAC AAAGTAGTAT 960
 TTTAGAAAAG TTCTAAAGTT ATAAAAATGT TTTCTGCACT AAAAAAAG TTCTCTGGGC 1020
 25 CGGGCGTGGT GGCTCACANC TGTAATCCCA GCACCTGGG AGGCTGAGGT GGGAGGATCA 1080
 TTTGAGGCCA GGAGTTTGAG ACCTGCCTGG GCAACATAAT GAACTTCCT TTCCAGGGAG 1140
 30 AAAAAAAAAA AAAAAAAAAA ACTCGA 1166

35 (2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 base pairs

(B) TYPE: nucleic acid

40 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

45 AGAGCGGACG AAGCTGGATA ACAGGGGACC GATGATGTGG CGACCATCAG TTCTGCTGCT 60
 TCTGTTGCTA CTGAGGCACG GGGCCAGGG GAAGCCATCC CCAGACGCAG GCCCTCATGG 120
 CCAGGGGAGG GTGCACCAGG CGGCCCCCT GAGCGACGCT CCCCATGATG ACGCCACGG 180
 50 GAACTTCCAG TACGACCATG AGGCTTTCCT GGGACGGGAA GTGGCCAAGG AATTGACCA 240
 ACTACCCCA GAGGAAAGCC AGGCCCTCT GGGGCGGATC GTGGACCGCA TGGACCGCGC 300
 55 GGGGACGGC GACGGCTGGG TGTCGCTGGC CGAGCTTCGC GCGTGGATCG CGCACACGCA 360
 GCAGCGGCAC ATACGGGACT CGGTGAGCGC GGCCTGGGAC ACGTACGACA CGGACCGCGA 420
 CGGGCGTGTG GGTGGGAGG AGCTGCGCAA CGYCACCTAT GGCCACTASG SGCCCGKTGA 480
 60

AGAATTTCAT GACGTGGAGG ATGCAGAGAC YTACAAAAAG ATGCTGGYTC GGGACGAGCG 540
GCGTTTCCGG GTGGCCGACC AGGATGGGGA CTCGATGGCC ACTCGA 586

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(2) INFORMATION FOR SEQ ID NO: 111:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

ACCCATTGAG CAGAAGGAGG CCAGGTGGGA AAGCTCCTGG GAAGAGCAGC CAGACTGGAC 60
20 ACTGGGCTGC TTGAGTCTCG AGTCACAATT CAGAATTCCT GGGCTCCCTG GGTGCATTCT 120
ATCATTCCAG TTGAAAGTTT GCTTCCTTCC AGTCATGTGG CTCTTCATTC TACTCTCCTT 180
GGCTCTCATT TCAGATGCCA TGGTCATGGA TGAAAAGGTC AAGAGAAGTT TGTGCTGGAC 240
25 ACGGCTTCTG CCATCTGCAA CTACAATGCC CAYTACAAGA ATCACCCCAA ATACTGGTGC 300
CGAGGYTATT TCCGTGAYTA CTGCAACATC ATCGCCTTCT CCCCTAACAG CACCAATCAT 360
30 GTGGCCCTGA AGGACACAGG GAACCAGCTC ATTGTCACTA TGTCTGCCT GAACAAANAA 420
GACACGGGCT GGTACTGGTG TGGCATCCAR CGGGACTTTG CMAGGGATGA CATGGATTTT 480
ACAGAGCTGA TTGTAAGTGA CGACAAAGGA ACCCTGGCCA ATGACTTTTG GTCTGGGAAA 540
35 GACCTATCAG GCAACAAAAC CAGAAGCTGC AAGGCTCCCA AAGTTGTCCG CAAGCTGACC 600
GCTCCAGGAC GTCCATTCTC ATCATTTGCA TACTGATCAC GGGTTTGGGA ATCATCTCTG 660
40 TAATCAGTCA TTTGACCAAA AGGAGGAGAA GTCAAAGGAA TAGAAGGGTA GGCAACACTT 720
TGAAGCCCTT CTCGCGTGTC CTGACTCCAA AGGAAATGGC TCCTACTGAA CAGATGTGAC 780
TGAAGWTTTT TTTAATTTAG TTNCATAAAG TGATGNCTAC AACAGAWTAA TCACCCATGA 840
45 CAACTGGCCC CACACCTCAG AGACTGATTC TGATCTCCCA GGAATCTCTGA AGGACCCCTCT 900
ATCCTTGACA ACAATCATTT GCAGCCAGGT AGCAACGGCR GTAGTCAGAG GAGCTATGAT 960
50 AGACCACACC CAAGCAAGGC TGCCCTCAAA TAACATCTCA AGATCTTAGT TCTTATGCAT 1020
TCCATCAGTC AGAAGTGAAG AAGAGGTGGA GAATCTKGAT TGGGGACCAG GAAATCACTT 1080
GTATTTTGTT AGCCAATAAA TTCCTAGCCA GTGTTGAATG AAAAAAAAAA AAAA 1134

55

(2) INFORMATION FOR SEQ ID NO: 112:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

10 CACTTTAAAG CTCTGCTGAG GGAGTTCGGA GCCCAGGCTT TCAGGCGACC TCTGCCCTCC 60
 CTGCCTCTCC TCACCCTCCC TCTCTTCCTG CAGGGCCTGG GAAGGGCTTT GAGGGAGCCT 120
 GGGAGCCATG TGAAGAGGGG CACGCCTGGG CTGTCCCACA GTTTAGATCC AGTTGGAGGT 180
 15 TCTCCCTGGC TCCTGCAGGC CTGCGGGGAT CTCTCCCCAC TTCAGGCCTC CGGCAGCTGC 240
 CTGCCCTCTT GTCTGTGCTT CAGCCCTGCA CAAAAGCAGC TTGGTGACAC CACTCAGCCA 300
 CCCAGAGTAC GTGTTTACAG GCTTTCAGTA TCACCTTCCT GTGGGGTGAA CGTAATGAGG 360
 20 CGGGGCTGGT CCTTGGAATT TCCCCTGGAA AATGGTAACA GACTCCATCC TTGACCCGGG 420
 GATGAGCATG AAGGCATTGT CCCAAAGGCA GAGGCCACCG TGGTAGGAAT TCCACCAAGG 480
 25 CCAGAAGGGA AAAAGGAAGA ACCCACCCTG TCTGGCTGTG CGGGCCCTGG GGAGGGTCGT 540
 GAGTGCAGCC CCTCTCTACT TCYGTGCCTT TGTA AACGT GTAGATAACC GCAGTGGTTG 600
 GCTGAGCCAA GAACTCTCCT AAATCAGTGG CTCTCTCCCC ACCCCTTGCT GGGGAGTCAT 660
 30 TTTTAAAAAA ATCTGTGGGA TATAAAATTG GCCTCCTGCT GCTTCAGCCT ACCTCTCCCT 720
 CTGCTGACTT AATGTCGTGA TTCGTCTTCT TCAGATAATT AAGGCTGTTA GGTGTGTGA 780
 35 GCCTTGAAGT GTGTGTGTGT GTCCCAGCGA CTGTCCACTG TCCAGGAGAT GCATGTCTTT 840
 GTATTGGAGA TATTTCTGTA ACTCATCTCT TTGGTGCTCA CGATTGCCAT GGCCATAGGG 900
 CCACAGTGCC GTATCTGCTG CAGACATGAT TGTCTCTTGT TCTAGAGGTT TTCTGTGTTT 960
 40 CGAATCTTGC CTGATGAATC CAGCCAGACC AAGGGGCCTA GATTTGACCT CTGTCCTGGG 1020
 CTCTTGGGCC AGGTGCAGGA ACATCTGAGG CCACTCTGCT GGCCACCTCC AGTGGGTGCT 1080
 45 GACCACAGGA TGGGCTTTGT TTACACTCAT TTTCACCCTG ATTCTTGCCC CCACTTTCAT 1140
 AAAAGAACT TCAAAATGCT GACGCTTTGG AGAGTAAGAA AATCAATCTT GGCTGGGCAC 1200
 GGTGGCTCCT GCTGTGATC CTAGCACTTT GGGAGGCTGA AGCTGAAGGA TCACTTGAGC 1260
 50 TCAGGAGTTG GAGACCAACC CTGGCAACAT AACAAGACCC TGTCTCTACA AAAAAAAAAA 1320
 AAAAAAACT CGA 1333

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(2) INFORMATION FOR SEQ ID NO: 113:

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(i) SEQUENCE CHARACTERISTICS:

262

- (A) LENGTH: 1015 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

GGCACGAGCG GCACGAGCGG CACGAGGTGA CTTCAAGTGT CGGATCTTTT CAGCCTACAT 60
 10 CAAGGAGGTG GAGGAACGGC CGGCACCCAC CCCGTGGGCT CCAAGATGCC CTTTGGGGAA 120
 CTGATGTTTC AATCCAGCAG TAGCTGCGGC TGGGTACATG GCGTCTGTTT CTCAGCCAGC 180
 GGGAGCCGCG TGGCCTGGGT AAGCCACGAC AGCACCGTCT GCCTGGCTGA TGCCGACAAG 240
 15 AAGATGGCCG TCGCGACTCT GGCCTCTGAA ACACTACCAC TGCTGGCGCT GACCTTCATC 300
 ACAGACAACA GCCTGGTGGC AGCGGGCCAC GACTGCTTCC CGGTGCTGTT CACCTATGAC 360
 20 GCCGCCGCGG GGATGCTGAG CTTCCGCGGG CGGCTGGACG TTCCTAAGCA GAGCTCGCAG 420
 CGTGGCTTGA CGGCCCCGCA GCGCTTCCAG AACCTGGACA AGAAGGCGAG CTCCGAGGGT 480
 GGCACGGCTG CGGGCGCGGG CCTAGACTCG CTGCACAAGA ACAGCGTCAG CCAGATCTCG 540
 25 GTGCTCAGCG GCGGCAAGGC CAAGTGCTCG CAGTTCTGCA CCACTGGCAT GGATGGCGGC 600
 ATGAGTATCT GGGATGTGAA GAGCTTGGAG TCAGCCTTGA AGGACCTCAA GATCAAATGA 660
 30 CCTGTGAGGA ATATGTTGCC TTCATCCTAG CTGCTGGGGA AGCGGGGAGA GGGGTCAGGG 720
 AGGCTAATGG TTGCTTTGCT GAATGTTTCT GGGGTACCAA TACGAGTTCC CATAGGGGCT 780
 GCTCCCTCAA AAAGGGAGGG GACAGATGGG GAGCTTTTCT TACCTATTCA AGGAATACGT 840
 35 GCCTTTTTCT TAAATGCTTT CATTTATTGA AAAAAAAAAA AAATGCCCCC AAAGCACTAT 900
 GCTGGTCATG AACTGCTTCA AAATGTGGAG GTAATAAAT GCAACTGTGT AAAAAAAAAA 960
 40 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACNC 1015

45

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

55 GGCACGAGGG GAAAGCCATG CTCCCAGGAC TCCTTCCTTG CAGCCTTAAA TCGGTCTGTA 60
 CGGAAATTC CGCGCCTTAG AAACCCACGC TTGGGTGTAA CTTATTATTG TTCTTCCTGA 120
 60 CCTACTTCCT GTTTATCACT TCCGGGTTC AATTTTGGC ATTTCCGTGA TCGGGTTGGA 180

ACTATTGAAG CCCGCTTTCA GGTCTTTTC CCCATTTTCC CTTTGAAAGG AAGACTTCTG 240
 GCTTCTCCTA AATCTCCGTT CTCTGGGTAA GGGGAGTCCA AGCCTCTGTC ATGAGGAACG 300
 5 GAAATGCGAG GGCCTCGGGT GTTACTCTAA AATCCGCCCT CAGCTTGCAC GCCGGAAGCT 360
 GCGATTCCCTG CAGCGGAAGA GGCCTGATCT GGCCTTCGAC TCGCTATGTC CACTAACAAT 420
 ATGTGCGACC CACGGAGGCC GAACAAAGTG CTGAGGTACA AGCCCCCGCC GAGCGAATGT 480
 10 AACCCGGCCT TGGACGACCC GACGCCGAC TACATGAACC TGCTGGGCAT GATCTTCAGC 540
 ATGTGCGGCC TCATGCTTAA GCTGAAGTGG TGTGCTTGGG TCGCTGCTA CTGCTCCTTC 600
 15 ATCAGCTTTG CCAACTCTCG GAGCTCGGAG GACACGAAGC AAATGATGAG TAGCTTCATG 660
 CTGTCCATCT CTGCCGTGGT GATGTCCTAT CTGCAGAATC CTCAGCCCAT GACGCCCCCA 720
 TGGTGATACC AGCCTAGAAG GGTACATTT TGGACCCTGT CTATCCACTA GGCCTGGGCT 780
 20 TTGGCTGCTA AACCTGCTGC CTTGAGCTGC CATCCTGGAC TTCCCTGAAT GAGGCCGTCT 840
 CGGTGCCCCC AGCTGGATAG AGGGAACCTG GCCCTTTCCT AGGGAACACC CTAGGCTTAC 900
 25 CCCTCCTGCC TCCCTTCCCC TGCCTGCTGC TGGGGGAGAT GCTGTCCATG TTTCTAGGGG 960
 TATTCATTTG CTTTCTCGTT GAAACCTGTT GTTAATAAAG TTTTTCACCT TGAAAAAANA 1020
 AAAAAAANA RAAACNCGN GGGGGGCCCC GGAACCCAAT TCSCCGGATA GTGAGT 1076
 30

(2) INFORMATION FOR SEQ ID NO: 115:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCGCTGCTGA TAACTATGGC ATCCCCCGGG CCTGCAGGAA TTCGGCACGG AGCTACGGCG 60
 45 CCGCCTGGCT CCTGCTGNCA CCTGCAGGCT CGTCGCGGGT GGAGCCCACC CAAGACATCA 120
 GCATCAGCGA CCAGCTGGGG GGCCAGGACG TGCCCGTGTT CCGGAACCTG TCCCTGCTGG 180
 50 TGGTGGGTGT CGGCGCCGTG TTCTCACTGC TATTCACCT GGGCACCCGG GAGAGGCGCC 240
 GGCCGCATGC GGASGAGCCA GGCGAGCACA CCCCCCTGTT GGCCCCTGCC ACGGCCAGC 300
 CCCTGCTGCT CTGGAAGCAC TGGCTCCGGG AGCSGGCTTT CTACCAGGTG GGCATACTGT 360
 55 ACATGACCAC CAGGCTCATC GTGAACCTGT CCCAGACCTA CATGGCCATG TACCTCACCT 420
 ACTCGCTCCA CCTGCCCCAAG AAGTTCATCG CGACCATTC CTTGGTGATG TACCTCAGCG 480
 60 GCTTCTTGTC CTCCTTCCTC ATGAAGCCCA TCAACAAGTG CATTGGGAGG AACATGACCT 540

5 ACTTCTCAGG CCTCCTGGTG ATCCTGGCCT TTGCCGCCTG GGTGGCGCTG GCGGAGGGAC 600
 TGGGTGTGGC CGTGACGCA GCGGCTGTGC TGCTGGGTGC TGGCTGTGCC ACCATCCTCG 660
 TCACCTCGCT GGCCATGACG GCCGACCTCA TCGGTCCCCA CACGAACAGC GGAGCKTTCG 720
 TGTACGGCTC CATGAGCTTC TTGGATAAGG TGGCCAATGG GCTGGCAGTC ATGGCCATCC 780
 10 AGAGCCTGCA CCCTTGCCCC TCAGAGCTCT GCTGCAGGGC CTGCGTGAGC TTTTACCACT 840
 GGGCGATGGT GGCTGTGACG GCGGCGGTGG GCGTGGCCGC TGCCCTGTGT CTCTGTAGCC 900
 TCCTGCTGTG GCCGACCCGC CTGCGACGCT GATGAGACCT GCACGCANTG GCTCACAGCA 960
 15 GCACGATTTG TGACAGCCCG AGGCGGAGAA CACCGAACAC CCACTGAAGG TGAGGGGATC 1020
 AGCACGGCGC GGCCACCCAC GCACCCACGC GCTGGAATGA GACTCAGCCA CAAGGAGGTG 1080
 20 CGAAGCTCTG ACCCAGGCCA CAGTGC GGAT GCACCTTGAG GATGTCACGC TCAGTGAGAG 1140
 ACACCAGACA CAGAAGGGTA CGTGTGATC CCACTTCTAT GAAATGTCCA GGACAGACCA 1200
 ATCCACAGAA TCAGGGAGAG GATTCTGTGG TGCCGGGACT GGGGAGGGGG ACCTGGGGGT 1260
 25 GACTAGGTGA CATAATGGGG ACAGGGCTGC CTTCTGGGTG ATGAGAATGT TCTGGAATCA 1320
 GATGGGATGG CTGCACGGCG TGGTGAAGGT ACTGAACGCC ACCTCACTGT AAGACGGTAG 1380
 30 ATTTTGTATT TTACCACAAT AAACAAAACA AAACAAACC AAAAAAAAAA AAAAAAAAAA 1440
 AAAAAAAGG AATTCGATAT CAAGCTTATC GATACCGTCG ACCTCGA 1487

35

(2) INFORMATION FOR SEQ ID NO: 116:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

GGCACGAGTG CGCANGCGTG GGGCTCTCTC CTGTGTCAGTC GCGCGCCGCT GCGGGCTGGT 60
 GGCTCTGTGG CAGCGGCGGC GGCAGGACTC CGGCACTATG AGCGGCTTCA GCACCGAGGA 120
 50 GCGCGCCGCG CCTTCTCCCT GGAGTACCGA GTCTTCCTCA AAAATGAGAA AGGACAATAT 180
 ATATCTCCAT TTCATGATAT TCCAATTTAT GCAGATAAGG ATGTGTTTCA CATGGTAGTT 240
 55 GAAGTACCAC GCTGGTCTAA TGCAAAAATG GAGATTGCTA CAAAGGACCC TTTAAACCCT 300
 ATTAACAAG ATGTGAAAAA AGGAAAACCT CGCTATGTTG CGAATTGTGT CCCGTATAAA 360
 GGATATATCT GGAACATATG TGCCATCCCT CAGACTTGGG AAGACCCAGG GCACAATGAT 420
 60

265

AAACATACTG GCTGTTGTGG TGACAATGAC CCAATTGATG TGTGTGAAAT TGGAAGCAAG 480
 GTATGTGCAA GAGGTGAAAT AATTGGCGTG AAAGTTCTAG GCATATTGGC TATGATTGAC 540
 5 GAAGGGGAAA CCGACTGGAA AGTCATTGCC ATTAATGTGG ATGATCCTGA TGCAGCCAAT 600
 TATAATGATA TCAATGATGT CAAACGGCTG AAACCTGGCT ACTTAGAAGC TACTGTGGAC 660
 10 TGGTTTAGAA GGTATAAGGT TCCTGATGGA AAACCAGAAA ATGAGTTTGC GTTTAATGCA 720
 GAATTTAAAG ATAAGGACTT TGCCATTGAT ATTATTAAAA GCACTCATGA CCATTGAAA 780
 GCATTAGTGA CTAAGAAAAC GAATGGAAAA GGAATCAGTT GCATGAATAC AACTTTGTCT 840
 15 GAGAGCCCCT TCAAGTGTGA TCCTGATGCT GCCAGAGCCA TTGTGGATGC TTTACCACCA 900
 CCCTGTGAAT CTGCCTGCAC AGTACCAACA GACGTGGATA AGTGGTTCCA TCACCAGAAA 960
 AACTAATGAG ATTTCTCTGG AATACAAGCT GATATTGCTA CATCGTGTTC ATCTGGATGT 1020
 20 ATTAGAAGTA AAAGTAGTAG CTTTTCAAAG CTTTAAATTT GTAGAACTCA TCTAACTAAA 1080
 GTAAATTCTG CTGTGACTAA TCCAATATAC TCAGAATGTT ATCCATCTAA AGCATTTTTC 1140
 25 ATATCTCAAC TAAGATAACT TTTAGCACAT GCTTAAATAT CAAAGCAGTT GTCATTGGA 1200
 AGTCACTTGT GAATAGATGT GCAAGGGGAG CACATATTGG ATGTATATGT TACCATATGT 1260
 TAGGAAATAA AATTATTTTG CTGAAAAAAA AAAAAAAAAA ACCTSGGGGG GGGSCCGGT 1320
 30 CCCCATTGG CCCTTTGGGG GGNGGTTTTA 1350

35

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2527 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

45 CTCTTGCTAC CTTCCCGGCG CAGAGAACCC CGGCTGCTCA GCGCGCTCCG GGGTCATGGA 60
 GATCCCCGGG AGCCTGTGCA AGAAAGTCAA GCTGAGCAAT AACGCGCAGA ACTGGGGAAT 120
 50 GCAGAGAGCA ACCAATGTCA CCTACCAAGC CCATCATGTC AGCAGGAACA AGAGAGGTCA 180
 GGTGGTGGGG ACCAGAGGTG GCTTTCGTGG TTGCACAGTT TGGCTAACAG GCTTGTCTGG 240
 AGCGGGAAAG ACTACTGTGA GCATGGCCTT GGAGGAGTAC CTGGTTTGTC ATGGTATTCC 300
 55 ATGCTACACT CTGGATGGTG ACAATATTCG TCAAGGTCTC AATAAAAATC TTGGCTTTAG 360
 TCCTGAAGAC AGAGAAGAGA ATGTTGACG CATCGCAGAA GTTGCTAAAC TGTTTGACAGA 420
 60 TGCTGGCTTA GTGTGCATCA CAAGTTTCAT ATCACCTTAC ACTCAGGATC GCAACAATGC 480

	AAGGCAAATT CATGAAGGTG CAAGTTTACC GTTTTTTGAA GTATTGTGTG ATGCTCCTCT	540
5	GCATGTTTGT GAACAGAGGG ATGTCAAAGG ACTCTACAAA AAAGCCCGGG CAGGAGAAAT	600
	TAAAGGTTTC ACTGGGATCG ATTCTGAATA TGAAAAGCCA GAGGCCCTG AGTTGGTGCT	660
	GAAAACAGAC TCCTGTGATG TAAATGACTG TGTCCAGCAA GTTGTGGAAC TTCTACAGGA	720
10	ACGGGATATT GTACCTGTGG ATGCATCTTA TGAAGTAAAA GAACTATATG TGCCAGAAAA	780
	TAAACTTCAT TTGGCAAAAA CAGATGCGGA AACATTACCA GCACTGAAAA TTAATAAAGT	840
15	GGATATGCAG TGGGTGCAGG TTTTGGCAGA AGGTTGGGCA ACCCCATTGA ATGGCTTTAT	900
	GAGAGAGAGG GAGTACTTGC AGTGCCTTCA TTTTGATTGT CTTCTGGATG GAGGTGTCAT	960
	TAACCTGTCA GTACCTATAG TTCTGACTGC GACTCATGAA GATAAAGAGA GGCTGGACGG	1020
20	CTGTACAGCA TTTGCTCTGA TGTATGAGGG CCGCCGTGTG GCCATTCTTC GCAATCCAGA	1080
	GTTTTTTGAG CACAGGAAAG AGGAGCGCTG TGCCAGACAG TGGGGAACGA CATGCAAGAA	1140
25	CCACCCCTAT ATTAAGATGG TGATGGAACA AGGAGATTGG CTGATTGGAG GAGATCTTCA	1200
	AGTCTTGGAT CGAGTTTATT GGAATGATGG TCTTGATCAG TATCGTCTTA CTCCTACTGA	1260
	GCTAAAGCAG AAATTTAAAG ATATGAATGC TGATGCTGTC TTTGCATTTT AACTACGCAA	1320
30	CCCAGTGCAC AATGGACATG CCCTGTTAAT GCAGGATACC CATAAGCAAC TTCTAGAGAG	1380
	GGGCTACCGG CGCCCTGTCC TCCTCCTCCA CCCTCTGGGT GGCTGGACAA AGGATGACGA	1440
35	TGTTCCTTTG ATGTGGCGTA TGAAGCAGCA TGCTGCAGTG TTGGAGGAAG GAGTTCTGAA	1500
	TCCTGAGACG ACAGTGGTGG CCATCTTCCC ATCTCCCATG ATGTATGCTG GACCAACTGA	1560
	GGTCCAGTGG CATTCGAGAG CACGGATGGT TGCAGGAGCC AACTTTTACA TTGTTGGACG	1620
40	AGACCCTGCT GGCATGCCTC ATCCAGAAAC AGGGAAGGAT CTTTATGAGC CAAGTCATGG	1680
	TGCCAAAGTG CTGACGATGG CCCCTGGTTT AATCACTTTG GAAATAGTTC CCTTTCGAGT	1740
45	TGCAGCTTAC AACAAGAAAA AGAAGCGTAT GGACTACTAT GACTCTGAAC ACCATGAAGA	1800
	CTTTGAATTT ATTTTCAGGAA CACGAATGCG CAAACTTGCT CGAGAAGGCC AGAAACCACC	1860
	TGAAGGTTTC ATGGCTCCCA AGGCTTGGAC CGTGCTGACA GAATACTACA AATCCTTGGA	1920
50	GAAAGCTTAG GCTGTTAACC CAGTCACTCC ACCTTTGACA CATTACTAGT AACAGAGGG	1980
	GACCACATAG TCTCTGTTGG CATTTCTTTG TGGTGTCTGT CTGGACATGC TTCCTAAAAA	2040
55	CAGACCATTT TCCTTAACTT GCATCAGTTT TGGTCTGCCT TATGAGTTCT GTTTTGAACA	2100
	AGTGTAACAC ACTGATGGTT TTAATGTATC TTTTCCACTT ATTATAGTTA TATTCCTACA	2160
	ATACAATTTT AAAATGTCT TTTTATATTA TATTTATGCT TCTGTGTCAT GATTTMTTCA	2220
60	AGCTGTTATA TTAGTTGTAA CCAGTAGTAT TCACATTAAA TCTTGCTTTT TTTCCCTTA	2280

5 AAAAAAGAAA AAAATTACCA AACAATAAAC TTGGCTAGAC CTGTGTTTGA GGATTTTACA 2340
 AGACCTTTGT AGCGATTAGA TTTTTTTTCT ACATTGAAAA TAGAACTGC TTCCTTTCTT 2400
 CTTTCCAGTC AGCTATTGGT CTTTCCAGCT GTTATAATCT AAAGTATTCT TATGATCTGT 2460
 GTAAGCTCTG AATGAACTTC TTTACTCAAT AAAATTAATT TTTTGGCTTC TTAAAAA 2520
 10 AAAAAA 2527

15 (2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1098 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

25 CGCATCACAG ACAACCCAGA AGGAAAATGG TTGGGCAGAA CAGCAAGGGG TTCATATGGC 60
 TATATTAAAA CAACTGCTGT AGAGATTNNC TATGATTCTT TGAAACTGAA AAAAGACTCT 120
 CTTGGTGCCC CTTCAAGACC TATTGAAGAT GACCAAGAAG TATATGATGA TGTTGCAGAG 180
 30 CAGGATGATA TTAGCAGCCA CAGTCAGAGT GGAAGTGGAG GGATATTCCC TCCACCACCA 240
 GATGATGACA TTTATGATGG GATTGAAGAG GAAGATGCTG ATGATGGTTT CCCTGCTCCT 300
 35 CCTAAACAAT TGGACATGGG AGATGAAGTT TACGATGATG TGGATACCTC TGATTTCCTT 360
 GTTTCATCAG CAGAGATGAG TCAAGGAACT AATGTTGGAA AAGCTAAGAC AGAAGAAAAG 420
 GACCTTAAGA AGCTAAAAAA GCAGRAAAAA GAARAAAAAG ACTTCAGGAA AAAATTTAAA 480
 40 TATGATGGTG AAATTAGAGT CCTATATTCA ACTAAAGTTA CAACTTCCAT AACTTCTAAA 540
 AAGTGGGGAA CCAGAGATCT ACAGGTAAAA CCTGGTGAAT CTCTAGAAGT TATACAAACC 600
 45 ACAGATGACA CAAAAGTTCT CTGCAGAAAT GAAGAAGGGA AATATGGTTA TGTCTTTCGG 660
 AGTTACCTAG CGGACAATGA TGGAGAGATC TATGATGATA TTGCTGATGG CTGCATCTAT 720
 GACAATGACT AGCACTCAAC TTTGGTCATT CTGCTGTGTT CATTAGGTGC CAATGTGAAG 780
 50 TCTGGATTTT AATTGGCATG TTATTGGGTA TCMAGAAAAT TAATGCACAR AACCACTTAT 840
 TATCATTTGT TATGAAATCC CAATTATCTT TACAAAGTGT TTAAAGTTTG AACATAGAAA 900
 55 ATAATCTCTC TGCTTAATTG TTATCTCAGA AGACTACATT AGTGAGATGT AAGAATTATT 960
 AAATATTCCT TTTCCGCTTT GGCTACAATT ATGAAGAAGT TGAAGGTACT TCTTTTAGAC 1020
 CACCAGTAAA TAATCCTCCT TCAAAAAATA AAAATAAAAA AAAAAAAAAA AACTCGAGG 1080
 60

GGGGGCCCCG TACCCAAT

1098

5

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 1679 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

15

TCGACCCACG CGTCCGGCGA GATCCCTACC GCAGTAGCCG CCTCTGCCGC CGCGGAGCTT 60

CCCGAACCTC TTCAGCCGCC CGGAGCCGCT CCCGGAGCCC GGCCGTAGAG GCTGCAATCG 120

20

CAGCCGGGAG CCCGCAGCCC GCGCCCCGAG CCCGCCGCCG CCCTTCGAGG GCGCCCCAGG 180

CCGCGCCATG GTGAAGGTGA CGTTCAACTC CGCTCTGGCC CAGAAGGAGG CCAAGAAGGA 240

25

CGAGCCCAAG AGCGGCAGAG AGGCGCTCAT CATCCCCCCC GACGCCGTCG CGGTGGACTG 300

CAAGGACCCA GATGATGTGG TACCAGTTGG CCAAAGAAGA GCCTGGTGTG GGTGCATGTG 360

CTTTGGACTA GCATTTATGC TTGCAGGTGT TATTCTAGGA GGAGCATACT TGTACAAATA 420

30

TTTTCGACTT CAACCAGATG ACGTGTACTA CTGTGGAATA AAGTACATCA AAGATGATGT 480

CATCTTAAAT GAGCCCTCTG CAGATGCCCC AGCTGTCTCT TACCAGACAA TTGAAGAAAA 540

TATTAAATC TTTGAAGAAG AAGAAGTTGA ATTTATCAGT GTGCCTGTCC CAGAGTTTGC 600

35

AGATAGTGAT CCTGCCAACA TTGTTTCATGA CTTTAACAAG AACTTTACAG CCTATTTAGA 660

TCTTAACCTG GATAAGTGCT ATGTGATCCC TCTGAACACT TCCATTGTGA TGCCACCCAG 720

40

AAACCTACTG GAGTTACTTA TTAACATCAA GGCTGGAACC TATTTGCCTC AGTCCTATCT 780

GATTCATGAG CACATGGTTA TTACTGATCG CATTGAAAAC ATTGATCACC TGGGTTTCTT 840

TATTTATCGA CTGTGTCATG ACAAGGAAAC TTACAACTG CAACGCAGAG AACTATTAA 900

45

AGGTATTTCAG AAACGTGAAG CCAGCAATTG TTTCGCAATT CGGCATTTTG AAAACAAATT 960

TGCCGTGGAA ACTTTAATTT GTTCTTGAAC AGTCAAGAAA AACATTATTG AGGAAAATTA 1020

50

ATATCACAGC ATAACCCAC CCTTTACATT TTGTGCAGTG ATTATTTTTT AAAGTCTTCT 1080

TTCATGTAAG TAGCAAACAG GGCTTTACTA TCTTTTCATC TCATTAATTC AATTAAAACC 1140

ATTACCTTAA AATTTTTTTC TTTCGAAGTG TGGTGTCTTT TATATTTGAA TTAGTAACTG 1200

55

TATGAAGTCA TAGATAATAG TACATGTCAC CTTAGGTAGT AGGAAGAATT ACAATTCTCT 1260

TAAATCATTT ATCTGGATTT TTATGTTTTA TTAGCATTTT CAAGAAGACG GATTATCTAG 1320

60

AGAATAATCA TATATATGCA TACGTAAAAA TGGACCACAG TGACTTATTT GTAGTTGTGA 1380

GTTGCCCTGC TACCTAGTTT GTTAGTGCAT TTGAGCACAC ATTTTAATTT TCCTCTAATT 1440
 AAAATGTGCA GTATTTTCAG TGTCAAATAT ATTTAACTAT TTAGAGAATG ATTTCCACCT 1500
 5 TTATGTTTTA ATATCCTAGG CATCTGCTGT AATAATATTT TAGAAAATGT TTGGAATTTA 1560
 AGAAATAACT TGTGTTACTA ATTTGTATAA CCCATATCTG TGCAATGGAA TATAAATATC 1620
 10 ACAAAGTTGT TTAAMWAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1679

15 (2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1308 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

25 TTGGCANCNG GGAGAGGGAA AGAGGAGGAA ATGGGGTTTG AGGACCATGG CTTACCTTTC 60
 CTGCCTTTGA CCCATCACAC CCCATTTCCT CCTCTTTCCC TCTCCCCGCT GCCAAAAAAA 120
 AAAAAAAGG AAACGTTTAT CATGAATCAA CAGGGTTTCA GTCCTTATCA AAGAGAGATG 180
 30 TGGAAAGAGC TAAAGAAACC ACCCTTTGTT CCCAACTCCA CTTTACCCAT ATTTTATGCA 240
 ACACAAACAC TGTCCCTTTG GGTCCCTTTC TTACAGATGG ACCTCTTGAG AAGAATTATC 300
 35 GTATTCCACG TTTTATAGCC TCAGGTTACC AAGATAAATA TATGTATATA TAACCTTTAT 360
 TATTGCTATA TCTTTGTGGA TAATACATTC AGGTGGTGCT GGGTGATTTA TTATAATCTG 420
 AACCTAGGTA TATCCTTTGG TCTTCCACAG TCATGTTGAG GTGGGCTCCC TGGTATGGTA 480
 40 AAAAGCCAGG TATAATGTAA CTTACCCCCA GCCTTTGTAC TAAGCTCTTG ATAGTGGATA 540
 TACTCTTTTA AGTTTATAGCC CAATATAGGG TAATGGAAAT TTCCTGCCCT CTGGGTTCCC 600
 45 CATTTTTACT ATTAAGAAGA CCAGTGATAA TTTAATAATG CCACCAACTC TGGCTTAGTT 660
 AAGTGAGAGT GTGAAGTGTG TGGCAAGAGA GCCTCACACC TCACTAGGTG CAGAGAGCCC 720
 AGGCCTTATG TTAAATCAT GCACTTGAAA AGCAAACCTT AATCTGCAA GACAGCAGCA 780
 50 AGCATTATAC GGTCACTCTG AATGATCCCT TTGAAATTTT TTTTGTGTTT GTTTGTTTAA 840
 ATCAAGCCTG AGGCTGGTGA ACAGTAGCTA CACACCCATA TTGTGTGTTT TGTGAATGCT 900
 55 AGCTCTCTTG AATTTGGATA TTGGTTATTT TTTATAGAGT GTAAACCAAG TTTTATATTC 960
 TGCAATGCCA ACAGGTACCT ATCTGTTTCT AAATAAACT GTTTACATTC ATTATGGGGT 1020
 ATGTATGACC TTCATTTTCC AAGAAATAGA ACTCTAGCTT AGAATTATGG ATGCTCTAAA 1080
 60

	ATGTCAGAAT GGGAACTCTC CTCGAAGTTC TCCCAAACCTC AGAGACAGCA CTGCCTTCTC	1140
	CTAAATGATT ATTCTTTTCT CCCTGTTTTC TGGTATTTTC TAGGCATCCT TCTCACCACA	1200
5	GCCATAACCC TTTTTTACTT CCATTAGGCC GTATAACTGG NGGGACNGCT GGTGCGTATA	1260
	TAATACTGGT WCCAACAMAG GGGTTCTGGA TGTACACMAG GTTATCTT	1308
10		
	(2) INFORMATION FOR SEQ ID NO: 121:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 1411 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:	
	GGCACAGGAG CGACCCGGGA GAAGGAGGGC CAMGAKGCGG AAGCGGAGGA GTCTCCAGGA	60
	GACCCGGGGA CAGCATCGCC CAGGCCCTTG TTTGCAGGCC TTTCAGATAT ATCCATCTCA	120
25	CAAGACATCC CCGTAGAAGG AGAAATCACC ATTCTATGA GATCTCGCAT CCGGGAGTTT	180
	GACAGCTCCA CATTAAATGA ATCTGTTTCG AATACCATCA TGCCTGATCT AAAAGCTGTT	240
30	GGGAAAAAAT TCATGCATGT TTTGTACCCA AGGAAAAGTA ATACTCTTTT GAGAGATTGG	300
	GATTTGTGGG GCCCTTTGAT CCTTTGTGTG AACTCGCAT TAATGCTGCA AAGAGACTCT	360
	GCAGATAGTG AAAAAGATGG AGGGCCCCAA TTTGCAGAGG TGTTTGTCAT TGTCTGGTTT	420
35	GGTGCAGTTA CCATCACCTT CAACTCAAAA CTTCCTGGAG GGAACATATC TTTTTTTCAG	480
	AGCCTCTGTG TGCTGGGTTA CTGTATACTT CCCTTGACAG TAGCAATGCT GATTTGCCGG	540
40	CTGGTACTTT TGGCTGATCC AGGACCTGTA AACTTCATGG TTCGGCTTTT TGTGGTGATT	600
	GTGATGTTTG CCTGGTCTAT AGTTGCCTCC ACAGCTTTCC TTGCTGATAG CCAGCCTCCA	660
	AACCGCAGAG CCCTAGCTGT TTATCTGTTT TTCCTGTTTT ACTTTGTCAT CAGTTGGATG	720
45	ATTCTCACCT TTAATCCTCA GTAAATCAGG AATGGGAAAT TAAAAACCAG TGAATTGAAA	780
	GCACATCTGA AAGATGCAAT TCACCATGGA GCTTTGTCTC TGGCCCTTAT TTGTCTAATT	840
50	TTGGAGGTAT TTGATAACTG AGTAGGTGAG GAGATTAAAA GGGAGCCATA TAGCACTGTC	900
	ACCCCTTATT TGAGGAACCTG ATGTTTGAAA GGCTGTTCTT TTCCTCTTTA ATGTCATTTT	960
55	TTTAAAAATA CATGTGCATA CTACACACAG TATATAATGC CTCCTTAAGG CATGATGGAG	1020
	TCACCGTGGT CCATTTGGGT GACAACCACT GACTTGGGAA GCACATAGAT ACATCTTACA	1080
	AGTTGAATAG AGTTGATAAC TATTTTCAGT TTTGAGAATA CCAGTTCAGG TGCAGCTCTT	1140
60	AAACACATTG CCTTATGACT ATTAGAATAT GCCTCTCTTT TCATAAATAA AAATACATGG	1200

TCTATATCCA TTTTCTTTTA TTTCTCTCTC TTAAGCTTAA AAAGGCAATG AGAGAGGTTA 1260
 GGAGTGGGTT CATAACCGGA GAATGAGAAA ACATGCATTA ACCAATATTC AGATTTTGAT 1320
 5 CAGGGGAAAT TCTAYACTTG TTGCAAAAAA AAAAAAAAAA AACTCGAGG GGGGCCCGGT 1380
 ACCCAATCGC NGTATATGAT CGNAAACAAT C 1411

10

(2) INFORMATION FOR SEQ ID NO: 122:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GCTTTGGCTT TTTTGGCGG ACTGGGGCGC CCTCCGGAAG CGTTCCTAAC TTTCCAGAAG 60
 25 TTTTCTCGGA CGGGCAGGAG GGGGTGGGGA CTGCCATATA TAGATCCCGG GAGCAGGGGA 120
 GCGGGCTAAG AGTAGAATCG TGTGCGGGCT CGAGAGCGAG AGTCACGTCC CGGCGCTAGC 180
 CAGCCCCACC CAGGCCACC GTGTGCACG CAAACCACTT CCTGGCCATG CGCTCCCTCC 240
 30 TGCTTCTCAG CGCCTTCTGC CTCCTGGAGG CGGCCCTGGC CGCCGAGGTG AAGAAACCTG 300
 CAGCCGCAGC AGCTCCTGGC ACTGCGGAGA AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG 360
 35 AGCGCANGCC GGCTGGCCT TCAGCTTGTA CCAGGCCATG GCCAAGGACC AGGCAGTGGA 420
 GAACATCTTG GTGTCACCCG TGGTGGTGGC CTCGTCGCTG GGGCTCGTGT CGCTGGGCGG 480
 CAAGGCGACC ACGGCGTCGC AGGCCAAGGC AGTGCTGAGC GCCGAGCAGC TGCGCGACGA 540
 40 GGAGGTGCAC GCCGGCCTGG GCGAGCTGCT GCGCTCACTC AGCAACTCGA CGGCGCGCAA 600
 CGTGACCTGG AAGCTGGGCA GCCGACTGTA CGGACCCAGC TCAGTGAGCT TCGCTGATGA 660
 45 CTTCGTGCGC ACAGCAAGCA GCACTACAAC TGCGAGCACT CCAAGATCAA CTTCGCGGAC 720
 AAGCGCAGNG CGCTGCAGTC CATCAACGAG TGGGCCGCGC AGACCACCGA CGGCAAGCTG 780
 CCCGAGGTCA CCAAGGACGT GGAGCGCACG GACGCGCCCC TGCTAGTCAA CGCCATGTTT 840
 50 TTCAAGCCAC ACTGGGATGA GAAATTCAC CACAAGATGG TGGACAACCG TGGCTTCATG 900
 GTGACTCGGT CCTATACYGT GGGTGTCTATG ATGATGCACC GGACAGGCCT CTACAACTAC 960
 55 TACGACGACG AGAAGGAAAA GCTGCAAATC GTGGAGATGC CCCTGGCCCA CAAGCTCTCC 1020
 AGCCTCATCA TCCTCATGCC CCATCACGTG GAGCCTCTCG AGCGCCTTGA AAAGCTGCTA 1080
 ACCAAAGAGC AGCTGAAGAT CTGGATGGGG AAGATGCAGA AGAAGGCTGT TGCCATCTCC 1140
 60

	TTGCCCAAGG GTGTGGTGGA GGTGACCCAT GACCTGCAGA AACACCTGGC TGGGCTGGGC	1200
	CTGACTGAGG CCATTGACAA GAACAAGGCC GACTTTRTCAC GCATGTCAGG CAAGAAGGAC	1260
5	CTGTACCTGG CCAGCGTGT CCACGCCACC GCCTTTGAGT TGGACACAGA TGGCAACCCC	1320
	TTTGACCAGG ACATCTACGG GCGCGAGGAG CTGCGCANCC CAAGCTGTTC TACGCCGACC	1380
10	ACCCCTTCAT CTTCTAGTG CGGACACCC AAAGCGGCTC CCTGCTATTC ATTGGGCGCC	1440
	TGGTCCGGCC TAAGGGTGAC AAGATGCGAG ACGAGTTATA GGGCCTCAGG GTGCACACAG	1500
	GATGGCAGGA GGCATCCAAA GGCTCCTGAG ACACATGGGT GCTATTGGGG TTGGGGGGGA	1560
15	GGTGAGGTAC CAGCCTTGA TACTCCATGG GGTGGGGGTG GAAAARCAGA CCGGGGTTC	1620
	CGTGTGCCTG AGCGGACCTT CCCAGCTAGA ATTCACTCCA CTTGGACATG GGCCCCAGAT	1680
20	ACCATGATGC TGAGCCCGGA AACTCCACAT CCTGTGGGAC CTGGGCCATA GTCATTCTGC	1740
	CTGCCCTGAA AGTCCCAGAT CAAGCCTGCC TCAATCAGTA TTCATATTTA TAGCCAGGTA	1800
	CCTTCTCACC TGTGAGACCA AATTGAGCTA GGGGGGTCAG CCAGCCCTCT TCTGACACTA	1860
25	AAACACCTCA GCTGCCTCCC CAGCTCTATC CCAACCTCTC CCAACTATAA AACTAGGTGC	1920
	TGCAGCCCCT GGGACCAGGC ACCCCCAGAA TGACCTGGCC GCAGTGAGGC GGATTGAGAA	1980
30	GGAGCTCCCA GGAGGGGCTT CTGGGCAGAC TCTGGTCAAG AAGCATCGTG TCTGGCGTTG	2040
	TGGGGATGAA CTTTTGTGTT TGTCTCTTCC TTTTTPAGTT CTTCAAAGAT AGGGAGGGAA	2100
	GGGGGAACAT GAGCCTTTGT TGCTATCAAT CCAAGAACTT ATTTGTACAT TTTTTTTTTC	2160
35	AATAAAACTT TTCCAATGAC AAAAAAAAAA AAAAAAAAAA AAAAAGGGGS GGGCCGCTCC	2220
	TAGAGGGATC CCTCCGANGG NGCCCAATCG AAAATN	2256

40

(2) INFORMATION FOR SEQ ID NO: 123:

- 45 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 829 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

	ATGCGCTCCC TCCTGCTTCT CAGCGCCTTC TGCCTCCTGG AGGCGGCCCT GGCCGCCGAG	60
55	GTGAAGAAAC CTGCAGCCGC AGCAGCTCCT GGCACTGCCG AGAAGTTGAG CCCCAGGCG	120
	GCCACGCTTG CCGAGCGCAA GCGGCCTGGC CTTCACTTGT TACCAGGCCA TGGCCAAGGA	180
	CCAGGCAGTG GAGAACATCC TGGTGTACCC CGTGGTGGTG GCCTCGTCGC TGGGGCTCGT	240
60	GTCGCTGGGC GGCAAGGCGA CCACGGCGTC GCAGGCCAAG GCAGTGCTGA GCGCCGAGCA	300

5 GCTGCGCGAC GAGGAGGTGC ACGCCGGCCT GGGCGAGCTG CTGCGCTCAC TCAGCAACTC 360
 CACGGCGCGC AACGTGACCT GGAAGCTGGG CAGCCGACTG TACGGACCCA GCTCAGTGAG 420
 CTTCGCTGAT GACTTCGTGC GCAGCAGCAA GCAGCACTAC AACTGCGAGC ACTCCAAGAT 480
 CAACTTCCGC GACAAGCGCA GCGCGCTGCA GTCCATCAAC GAGTGGGCCG CGCAGACCAC 540
 10 CGACGGCAAG CTGCCCAGG TCACCAAGGA CGTGGAGCGC ACGGACGGCG CCCTGTTAGT 600
 CAACGCCATG TTCTTCAAGC CACACTGGGA TGAGAAATTC CACCACAAGA TGGTGGACAA 660
 CCGTGGCTTC ATGGTGACTC GGTCTTATAC CGTGGGTGTC ATGATGATGC ACCGGACAGG 720
 15 CCTCTACAAC TACTACGACG ACGAGAAGGA AAAGCTGCAA ATCGTGGAGA TGCCCCTGGC 780
 CCACAAGCTC TCCAGCCTCA TCATCCTCAT GCCCCATCAC GTGGAGCCT 829

20

(2) INFORMATION FOR SEQ ID NO: 124:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

CCTCCGGAAG CGTTTCCAAC TTTCCAGAAG TTTCTCGGGA CGGGCAGGAG GGGGTGGGGA 60
 35 CTGCCATATA TAGATCCCGG GAGCAGGGGA GCGGGCTAAG AGTAGAATCG TGTCGCGGCT 120
 CGAGAGCGAG AGTCACGTCC CGGCGCTAGC CAGCCCGACC CAGGCCCACC GTGGTGCACG 180
 40 CAAACCACTT CCTGGCCATG CGCTCCCTCC TGCTTCTCAG CGCCTTCTGC CTCCTGGAGG 240
 CGGCCCTGGC CGCCGAGGTG AAGAAACCTG CAGCCGCAGC AGCTCCTGGC ACTGCGGAGA 300
 AGTTGAGCCC CAAGGCGGCC ACGCTTGCCG AGCGCAGNCG GCCTGGCCTT CAGCTTGATC 360
 45 CAGGCCATGG CCAAGGACCA GGCAGTGGAG AACATCCTGG TGTCACCCGT GGTGGTGGCC 420
 TCGTCGCTGG GGCTCGTGTC GCTGGGCGGC AAGGCGACCA CGGCGTCGCA GGCCAAGGCA 480
 GTGCTGAGCG CCGAGCAGCT GCGCGACGAG GAGGTGCACG CCGGCCTGGG CGAGCTGCTG 540
 50 CGCTCACTCA GCAACTCSAC GCGCGCAAC GTGACCTGGA AGCTGGGCAG CCGACTGTAC 600
 GGACCCAGCT CAGTGAGCTT CGCTGATGAC TTCGTGCGCA CAGCAAGCAG CACTACAAC 660
 55 GCGAGCACTC CAAGATCAAC TTCCGCGACA AGCGCACGCG CTGCAGTCCA TCAACGAGTG 720
 GGCCGCGCAG ACCACCGACG GCAAGCTGCC CGAGGTCACC AAGGACGTGG AGCGCACGGA 780
 CGGCGCCCTG YTAGTCAACG CCATGTTCTT CAAGCCACAC TGGGATGAGA AATTCCACCA 840

60

	CAAGATGGTG GACAACCGTG GCTTCATGGT GACTCGGTCC TATACYGTGG GTGTCATGAT	900
	GATGCACCGG ACAGGCCTCT ACAACTACTA CGACGACGAG AAGGAAAAGC TGCAAATCGT	960
5	GGAGATGCC CTGCCCCACA AGCTCTCCAG CCTCATCATC CTCATGCCCC ATCACGTGGA	1020
	GCCTCTCGAG CGCCTTGAAA AGCTGCTAAC CAAAGAGCAG CTGAAGATCT GGATGGGGAA	1080
10	GATGCAGAAG AAGGCTGTTG CCATCTCCTT GCCCAAGGGT GTGGTGGAGG TGACCCATGA	1140
	CCTGCAGAAA CACCTGGCTG GGCTGGGCCT GACTGAGGCC ATTGACAAGA ACAAGGCCGA	1200
	CTTRTCACGC ATGTCAGGCA AGAAGGACCT GTACCTGGCC AGCGTGTTC ACGCCACCGC	1260
15	CTTTGAGTTG GACACAGATG GCAACCCCTT TGACCAGGAC ATCTACGGGC GCGAGGAGCT	1320
	GCGCASCCEA AGCTGTTCTA CGCCGACCAC CCCTTCATCT TCCTAGTGCG GGACACCCAA	1380
20	AGCGGCTCCC TGCTATTCAT TGGGCGCCTG GTCCGGCCTA AGGGTGACAA GATGCGAGAC	1440
	GAGTTATAGG GCCTCAGGGT GCACACAGGA TGGCAGGAGG CATCCAAAGG CTCCTGAGAC	1500
	ACATGGGTGC TATTGGGGTT GGGGGGGAGG TGAGGTACCA GCCTTGGATA CTCCATGGGG	1560
25	TGGGGGTGGA AAARCAGACC GGGGTTCCTG TGTGCCTGAG CGGACCTTCC CAGCTAGAAT	1620
	TCACTCCACT TGGACATGGG CCCCAGATAC CATGATGCTG AGCCCGGAAA CTCCACATCC	1680
30	TGTGGGACCT GGGCCATAGT CATTCCTGCTT GCCCTGAAAG TCCCAGATCA AGCCTGCCTC	1740
	AATCAGTATT CATATTTATA GCCAGGTACC TTCTCACCTG TGAGACCAA TTGAGCTAGG	1800
	GGGGTCAGCC AGCCCTCTTC TGACACTAAA ACACCTCAGC TGCTTCCCA GCTCTATCCC	1860
35	AACCTCTCCC AACTATAAAA CTAGGTGCTG CAGCCCCTGG GACCAGGCAC CCCCAGAATG	1920
	ACCTGGCCGC AGTGAGGCGG ATTGAGAAGG AGCTCCAGG AGGGGCTTCT GGGCAGACTC	1980
40	TGGTCAAGAA GCATCGTGTC TGGCGTTGTG GGGATGAACT TTTTGTTTTG TTTCTTCCTT	2040
	TTTTAGTTCT TCAAAGATAG GGAGGGAAGG GGGAACATGA GCCTTTGTTG CTATCAATCC	2100
	AAGAACTTAT TTGTACATTT TTTTTCCTCA TAAACTTTT CCAATGACAA AAAAAAAAAA	2160
45	AAAAAAAAA MWMGGGSGG GCCGCTCCTA GAGGGATCCC TCCGANGNG CCCAATCGAA	2220
	AAT	2223

50

(2) INFORMATION FOR SEQ ID NO: 125:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

60

Met Lys Lys Gln Ser Lys Arg Cys Leu Trp Lys Pro Pro Gly Ser Leu

275

1 5 10 15
 Arg Arg Leu Trp Trp Met Arg Ala Leu Leu Ile Leu Lys Tyr Ile
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 126:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

15

Met Lys Lys Ser Leu Glu Asn Leu Asn Arg Leu Gln Val Met Leu Leu
 1 5 10 15

20

His Leu Thr Ala Ala Phe Leu Gln Arg Ala His Xaa Ile Leu Thr Thr
 20 25 30

Arg Met Ser Leu Gly Phe Gln Ser Pro His Leu Thr Met
 35 40 45

25

(2) INFORMATION FOR SEQ ID NO: 127:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

35

Met His Asn Gln Arg Gln Val Phe Leu Phe His Leu Phe Ser Asn Tyr
 1 5 10 15

40

Leu Leu Ser Ile Asn Ser Val Pro Gly Thr Leu Leu Ala Ala Thr Tyr
 20 25 30

Cys Leu Asn Met Thr Tyr Gly
 35

45

(2) INFORMATION FOR SEQ ID NO: 128:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

55

Met Arg Lys Lys Phe Leu Leu Ala Gln Val Phe Leu Ser Leu Ser Val
 1 5 10 15

Met Pro Ser Met Pro Val Thr
 20

60

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

10 Met Val Leu Leu Cys Leu Leu Leu Val Pro Leu Leu Leu Ser Leu Phe
 1 5 10 15
 Val Leu Gly Leu Phe Leu Trp Phe Leu Lys Arg Glu Arg Gln Glu Glu
 20 25 30
 15 Tyr Ile Glu Glu Lys Lys Arg Val Asp Ile Cys Arg Glu Thr Pro Asn
 35 40 45
 Ile Cys Pro His Ser Gly Glu Asn Thr Glu Tyr Asp Thr Ile Pro His
 20 50 55 60
 Thr Asn Arg Thr Ile Leu Lys Glu Asp Pro Ala Asn Thr Val Tyr Ser
 65 70 75 80
 25 Thr Val Glu Ile Pro Lys Lys Met Glu Asn Pro His Ser Leu Leu Thr
 85 90 95
 Met Pro Asp Thr Pro Arg Leu Phe Ala Tyr Glu Asn Val Ile
 100 105 110
 30

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

40 Met Leu Leu Leu Phe Ile Tyr Phe Tyr Ser His Pro Ala Pro Val Pro
 1 5 10 15
 Ala Gly Ala Thr Ser Lys Pro Arg Tyr Arg Val Ile Thr Cys Gly Pro
 45 20 25 30
 Ala Ser Val Phe Ser Thr Ser Phe Ser His Ser Pro Pro Ala Arg Cys
 35 40 45
 50 Leu Gly Arg Leu Glu Gln Met Phe His Phe Gly Leu Ala Ser Gly
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Met Pro Phe Pro Ile Ser Ile Leu Gln Leu Cys Leu Gln Ile Ser Asn
 1 5 10 15
 5 Leu Ser Phe Cys Leu Gln Lys Ile Tyr Lys Ile Pro Phe Val
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Met Ala Ala Ala Cys Arg Ser Val Lys Gly Leu Val Ala Val Ile Thr
 1 5 10 15
 Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Asp Asp Leu Trp Gly
 20 25 30
 25 Arg Glu Pro Leu Leu Cys Phe Trp Thr Cys Pro Thr Arg Val Gly Arg
 35 40 45
 Pro Lys Pro Arg Ser
 50

30

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Met Leu Leu Val Tyr Asp Leu Tyr Leu Xaa Pro Lys Leu Trp Ala Leu
 1 5 10 15
 45 Ala Thr Pro Gln Lys Asn Gly Lys Gly Ala Arg Xaa Gly Asp Gly Thr
 20 25 30
 Pro Ala Gln Ala Phe Trp Asp Phe Trp Ser His Leu Ile Ser Ala Asp
 35 40 45
 50 Pro Gln Thr Trp Glu Arg Ala Ala Pro
 50 55

55

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

5 Met Arg Leu Ser Ala Leu Leu Ala Leu Ala Ser Lys Val Thr Leu Pro
 1 5 10 15
 Pro His Tyr Arg Tyr Gly Met Ser Pro Pro Gly Ser Val Ala Asp Lys
 20 25 30
 10 Arg Lys Asn Pro Pro Trp Ile Arg Arg Arg Pro Val Val Val Glu Pro
 35 40 45
 Ile Ser Asp Glu Asp Trp Tyr Leu Phe Cys Gly Asp Thr Val Glu Ile
 50 55 60
 15 Leu Glu Gly Lys Asp Ala Gly Lys Gln Gly Lys Val Val Gln Val Ile
 65 70 75 80
 Arg Gln Arg Asn Trp Val Val Val Gly Gly Leu Asn Thr His Tyr Arg
 85 90 95
 20 Tyr Ile Gly Lys Thr Met Asp Tyr Arg Gly Thr Met Ile Pro Ser Glu
 100 105 110
 Ala Pro Leu Leu His Arg Gln Val Lys Leu Val Asp Pro Met Asp Arg
 115 120 125
 25 Lys Pro Thr Glu Ile Glu Trp Arg Phe Thr Glu Ala Gly Glu Arg Val
 130 135 140
 30 Arg Val Ser Thr Arg Ser Gly Arg Ile Ile Pro Lys Pro Glu Phe Pro
 145 150 155 160
 Arg Ala Asp Gly Ile Val Pro Glu Thr Trp Ile Asp Gly Pro Lys Asp
 165 170 175
 35 Thr Ser Val Glu Asp Ala Leu Glu Arg Thr Tyr Val Pro Cys Leu Lys
 180 185 190
 40 Thr Leu Gln Glu Glu Val Met Glu Ala Met Gly Ile Lys Glu Thr Arg
 195 200 205
 Lys Tyr Lys Lys Val Tyr Trp Tyr
 210 215

45

(2) INFORMATION FOR SEQ ID NO: 135:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

55 Met Ser Leu Arg Gln Lys Ser Ser Phe Arg Leu Met Val Met Ser Leu
 1 5 10 15
 Thr Ile Leu Lys Leu Ser Lys Thr Thr Val Leu Cys Leu Arg Cys Leu
 20 25 30

60

His Ser Leu Lys Leu Thr Trp Arg Asp Gly Ala Arg Cys Ile Asn Ala
 35 40 45

Glu

5

(2) INFORMATION FOR SEQ ID NO: 136:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Met Ser Gly Ser Phe Ile Leu Cys Leu Ala Leu Val Thr Arg Trp Ser
 1 5 10 15

20

Pro Gln Ala Ser Ser Val Pro Leu Ala Val Tyr Glu Ser Lys Thr Arg
 20 25 30

Lys Ser Tyr Arg Ser Gln Arg Asp Arg Asp Gly Lys Asp Arg Ser Gln
 35 40 45

25

Gly Met Gly Leu Ser Leu Leu Val Glu Thr Arg Lys Leu Leu Leu Ser
 50 55 60

Ala Asn Gln Gly
 65

30

(2) INFORMATION FOR SEQ ID NO: 137:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Met Cys Phe Arg Phe Phe Leu Phe Cys Ser Arg Ile Leu Leu Lys Leu
 1 5 10 15

45

Phe Phe Leu Leu Phe Pro Ala Ser Ala Phe Pro Leu Ser Thr Arg Ser
 20 25 30

Ser Leu Ser Val Asn Glu His Val Val Val Ser Pro Arg Ser Thr Val
 35 40 45

50

Ser Ile Ser Arg
 50

55

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 541 amino acids

60

(B) TYPE: amino acid

280

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

5 Met Val Arg Thr Asp Gly His Thr Leu Ser Glu Lys Arg Asn Tyr Gln
 1 5 10 15
 Val Thr Asn Ser Met Phe Gly Ala Ser Arg Lys Lys Phe Val Glu Gly
 20 25 30
 10 Val Asp Ser Asp Tyr His Asp Glu Asn Met Tyr Tyr Ser Gln Ser Ser
 35 40 45
 Met Phe Pro His Arg Ser Glu Lys Asp Met Leu Ala Ser Pro Ser Thr
 50 55 60
 15 Ser Gly Gln Leu Ser Gln Phe Gly Ala Ser Leu Tyr Gly Gln Gln Ser
 65 70 75 80
 Ala Leu Gly Leu Pro Met Arg Gly Met Ser Asn Asn Thr Pro Gln Leu
 85 90 95
 20 Asn Arg Ser Leu Ser Gln Gly Thr Gln Leu Pro Ser His Val Thr Pro
 100 105 110
 25 Thr Thr Gly Val Pro Thr Met Ser Leu His Thr Pro Pro Ser Pro Ser
 115 120 125
 Arg Gly Ile Leu Pro Met Asn Pro Xaa Asn Met Met Asn His Ser Gln
 130 135 140
 30 Val Gly Gln Gly Ile Gly Ile Pro Ser Arg Thr Asn Ser Met Ser Ser
 145 150 155 160
 Ser Gly Leu Gly Ser Pro Asn Arg Ser Ser Pro Ser Ile Ile Cys Met
 165 170 175
 35 Pro Lys Gln Gln Pro Ser Arg Gln Pro Phe Thr Val Asn Ser Met Ser
 180 185 190
 40 Gly Phe Gly Met Asn Arg Asn Gln Ala Phe Gly Met Asn Asn Ser Leu
 195 200 205
 Ser Ser Asn Ile Phe Asn Gly Thr Asp Gly Ser Glu Asn Val Thr Gly
 210 215 220
 45 Leu Asp Leu Ser Asp Phe Pro Ala Leu Ala Asp Arg Asn Arg Arg Glu
 225 230 235 240
 Gly Ser Gly Asn Pro Thr Pro Leu Ile Asn Pro Leu Ala Gly Arg Ala
 245 250 255
 50 Pro Tyr Val Gly Met Val Thr Lys Pro Ala Asn Glu Gln Ser Gln Asp
 260 265 270
 55 Phe Ser Ile His Asn Glu Asp Phe Pro Ala Leu Pro Gly Ser Ser Tyr
 275 280 285
 Lys Asp Pro Thr Ser Ser Asn Asp Asp Ser Lys Ser Asn Leu Asn Thr
 290 295 300
 60

281

Ser Gly Lys Thr Thr Ser Ser Thr Asp Gly Pro Lys Phe Pro Gly Asp
 305 310 315 320
 5 Lys Ser Ser Thr Thr Gln Asn Asn Asn Gln Gln Lys Lys Gly Ile Gln
 325 330 335
 Val Leu Pro Asp Gly Arg Val Thr Asn Ile Pro Gln Gly Met Val Thr
 340 345 350
 10 Asp Gln Phe Gly Met Ile Gly Leu Leu Thr Phe Ile Arg Ala Ala Glu
 355 360 365
 Thr Asp Pro Gly Met Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr
 370 375 380
 15 Leu Gly Leu Asn Leu Asn Ser Pro Glu Asn Leu Tyr Pro Lys Phe Ala
 385 390 395 400
 20 Ser Pro Trp Ala Ser Ser Pro Cys Arg Pro Gln Asp Ile Asp Phe His
 405 410 415
 Val Pro Ser Glu Tyr Leu Thr Asn Ile His Ile Arg Asp Lys Leu Ala
 420 425 430
 25 Ala Ile Lys Leu Gly Arg Tyr Gly Glu Asp Leu Leu Phe Tyr Leu Tyr
 435 440 445
 Tyr Met Asn Gly Gly Asp Val Leu Gln Leu Leu Ala Ala Val Glu Leu
 450 455 460
 30 Phe Asn Arg Asp Trp Arg Tyr His Lys Glu Glu Arg Val Trp Ile Thr
 465 470 475 480
 Arg Ala Pro Gly Met Glu Pro Thr Met Lys Thr Asn Thr Tyr Glu Arg
 485 490 495
 Gly Thr Tyr Tyr Phe Phe Asp Cys Leu Asn Trp Arg Lys Val Ala Lys
 500 505 510
 40 Glu Phe His Leu Glu Tyr Asp Lys Leu Glu Glu Arg Pro His Leu Pro
 515 520 525
 Ser Thr Phe Asn Tyr Asn Pro Ala Gln Gln Ala Phe Xaa
 530 535 540
 45

(2) INFORMATION FOR SEQ ID NO: 139:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Met Ile Cys Pro Gln Cys Pro Leu Ser Leu Leu Cys Leu Ile Ser Ser
 1 5 10 15
 60 Leu Cys Ser Leu Val Ile Gln Ile Ser Leu Lys Thr Ile Arg Asp Ile
 20 25 30

Thr Leu Leu Asn Met Val Gly Ile Lys Phe Ser Ile Ser Leu Ser Asn
 35 40 45

5 Lys Ile Asn Ile Asn Ser Arg Thr Trp Xaa
 50 55

10 (2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Met Thr Leu Arg Pro Ser Leu Leu Pro Leu His Leu Leu Leu Leu Leu
 1 5 10 15

20 Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu Thr Glu
 20 25 30

25 Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu Pro Pro Glu
 35 40 45

Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu His Ile His Tyr
 50 55 60

30 Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg
 65 70 75 80

Asp Pro Leu Val Ile Glu Leu Gly Gln Lys Gln Val Ile Pro Gly Leu
 85 90 95

35 Glu Gln Ser Leu Leu Asp Met Cys Val Gly Glu Lys Arg Arg Ala Ile
 100 105 110

Ile Pro Ser His Leu Ala Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val
 115 120 125

40 Pro Ala Asp Ala Val Val Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile
 130 135 140

45 Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys Gly Ile Leu Pro Leu Val
 145 150 155 160

Gly Met Ala Met Val Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu
 165 170 175

50 Tyr Arg Lys Ala Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu
 180 185 190

55 Glu Lys Arg Asn Lys Ser Lys Lys Lys Xaa
 195 200

60 (2) INFORMATION FOR SEQ ID NO: 141:

283

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Met Phe Leu Arg Leu Tyr Leu Ile Ala Arg Val Met Leu Leu His Ser
 1 5 10 15

10 Lys Leu Phe Thr Asp Ala Ser Ser Arg Ser Ile Gly Ala Leu Asn Lys
 20 25 30

Ile Asn Phe Asn Thr Arg Phe Val Met Lys Thr Leu Met Thr Ile Cys
 35 40 45

15 Pro Gly Thr Val Leu Leu Val Phe Ser Ile Ser Leu Trp Ile Ile Ala
 50 55 60

Ala Trp Thr Val Arg Val Cys Glu Ser Pro Glu Ser Pro Ala Gln Pro
 20 65 70 75 80

Ser Gly Ser Ser Leu Pro Ala Trp Tyr His Asp Gln Gln Asp Val Thr
 85 90 95

25 Ser Asn Phe Leu Gly Ala Met Trp Leu Ile Ser Ile Thr Phe Leu Ser
 100 105 110

Ile Gly Tyr Gly Asp Met Val Pro His Thr Tyr Cys Gly Lys Gly Val
 115 120 125

30 Cys Leu Leu Thr Gly Ile Met Gly Ala Gly Cys Thr Ala Leu Val Val
 130 135 140

Ala Val Val Ala Arg Lys Leu Glu Leu Thr Lys Ala Glu Lys His Val
 35 145 150 155 160

His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Ile Lys Asn Ala
 165 170 175

40 Ala Ala Asn Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys His Thr Lys
 180 185 190

Leu Leu Lys Lys Ile Asp His Ala Lys Val Arg Lys His Gln Arg Lys
 195 200 205

45 Phe Leu Pro Ser Tyr Pro Pro Val Xaa
 210 215

50

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

60 Met Ser Asn Thr Thr Val Pro Asn Ala Pro Gln Ala Asn Ser Asp Ser
 1 5 10 15

284

Met Val Gly Tyr Val Leu Gly Pro Phe Phe Leu Ile Thr Leu Val Gly
 20 25 30

5 Val Val Val Ala Val Val Met Tyr Val Gln Lys Lys Lys Arg Val Asp
 35 40 45

Arg Leu Arg His His Leu Leu Pro Met Tyr Ser Tyr Asp Pro Ala Glu
 50 55 60

10 Glu Leu His Glu Ala Glu Gln Glu Leu Leu Ser Asp Met Gly Asp Pro
 65 70 75 80

15 Lys Val Val His Gly Trp Gln Ser Gly Tyr Gln His Lys Arg Met Pro
 85 90 95

Leu Leu Asp Val Lys Thr
 100

20

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

30 Met Arg Glu Cys Gln Glu Glu Ser Phe Trp Lys Arg Ala Leu Pro Phe
 1 5 10 15

Ser Leu Val Ser Met Leu Val Thr Gln Gly Leu Val Tyr Gln Gly Tyr
 20 25 30

35 Leu Ala Ala Asn Ser Arg Phe Gly Ser Leu Pro Lys Val Ala Leu Ala
 35 40 45

40 Gly Leu Leu Gly Phe Gly Leu Gly Lys Val Ser Tyr Ile Gly Val Cys
 50 55 60

Gln Ser Lys Phe His Phe Phe Glu Asp Gln Leu Arg Gly Ala Gly Phe
 65 70 75 80

45 Gly Pro Gln His Asn Arg His Cys Leu Leu Thr Cys Glu Glu Cys Lys
 85 90 95

Ile Lys His Gly Leu Ser Glu Lys Gly Asp Ser Gln Pro Ser Ala Ser
 100 105 110

50

55

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:
 60 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid

285

(D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

5 Met Lys Asn Asp Arg Asn Gln Gly Phe Ser Leu Leu Gln Leu Ile Asp
 1 5 10 15
 Trp Asn Lys Pro
 20

10

(2) INFORMATION FOR SEQ ID NO: 145:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

20 Met Gly Thr Gln Pro Pro Val Val Ala Gly Phe Thr Ile Pro Met Leu
 1 5 10 15
 Gly Tyr Thr Val Arg Val Leu Thr Phe His Leu Ser Cys Ser
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 146:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

35

Met Lys Ile Pro Val Leu Pro Ala Val Val Leu Leu Ser Leu Leu Val
 1 5 10 15

40

Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu Glu Ser
 20 25 30

Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn Thr Pro Phe
 35 40 45

45

Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala Asp Glu Phe Leu
 50 55 60

50

Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg Lys Leu Pro Phe Leu
 65 70 75 80

Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly Leu Arg Ser Ala Thr Pro
 85 90 95

55

Asp Ala Gln

60

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Met Val Trp Gly Leu Leu Gly
 1 5

10

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

20 Met Leu Pro Leu Leu Ser Leu Leu Phe Leu Phe Phe Ser Thr Val Ser
 1 5 10 15

Ser Phe Cys Gly Met Pro Leu Arg Ala His Thr Arg Ala Xaa Ala His
 20 25 30

25

Thr Arg Thr Phe Ala Ser Arg
 35

30

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

40 Met Ile Cys Glu Thr Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg
 1 5 10 15

Leu Pro Pro Pro Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr
 20 25 30

45 Ile Glu Arg Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp
 35 40 45

Leu Pro Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile
 50 55 60

50

Ile Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 65 70 75 80

55

Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro Ser
 85 90 95

Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His Gln Ala
 100 105 110

60

Val Asp Ser Pro Thr Ser Val Ala Ser Val Asp Gly Pro Val Leu Met

115 120 125

Gly Ser Thr
130

5

(2) INFORMATION FOR SEQ ID NO: 150:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

15 Met Gly Ala Pro Ser Leu Thr Met Leu Leu Leu Lys Val Gln Pro
 1 5 10 15

20 Arg Arg Thr Gln Ala Phe Asp Ala His Trp Val Gly Leu Pro Leu Leu
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 151:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

35 Met Cys Leu Ile Phe Leu Leu Leu Leu Leu Ser Phe Ser
 1 5 10

40 (2) INFORMATION FOR SEQ ID NO: 152:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

 His Pro His Gln Asp Ser Gln Pro
 1 5

50

(2) INFORMATION FOR SEQ ID NO: 153:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

60

288

Met Asn Thr Ser Tyr Ile Leu Arg Leu Thr Val Val Val Ser Val Val
 1 5 10 15

Ile Tyr Leu Ala Ile His Pro Leu Leu Ser Phe Ser Leu Glu Ser Pro
 20 25 30

Leu Leu Val Pro Trp Arg Asp Cys Cys Gln Asn Ile Trp Lys Ser Gly
 35 40 45

Ser Val Trp Tyr Lys Arg Trp Thr Leu Pro His Met Glu Val Cys Cys
 50 55 60

Gln Asp Leu His
 65

15

(2) INFORMATION FOR SEQ ID NO: 154:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

25

Met Leu Lys Ile Phe Lys Glu Trp Glu Asn Leu Asn Leu Ile Leu Thr
 1 5 10 15

30

Ser Ile Arg Ile Leu Glu Arg Gln Asn Met
 20 25

(2) INFORMATION FOR SEQ ID NO: 155:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

40

Met Asp Cys Glu Val Asn Asn Gly Ser Ser Leu Arg Asp Glu Cys Ile
 1 5 10 15

45

Thr Asn Leu Leu Val Phe Gly Phe Leu Gln Ser Cys Ser Asp Asn Ser
 20 25 30

Phe Arg Arg Glu Leu Asp Ala Leu Gly His Glu Leu Pro Val Leu Ala
 35 40 45

50

Pro Gln Trp Glu Gly Tyr Asp Glu Leu Gln Thr Asp Gly Asn Arg Ser
 50 55 60

55

Ser His Ser Arg Leu Gly Arg Ile Glu Ala Asp Ser Glu Ser Gln Glu
 65 70 75 80

Asp Ile Ile Arg Asn Ile Ala Arg His Leu Ala Gln Val Gly Asp Ser
 85 90 95

60

Met Asp Arg Ser Ile Pro Pro Gly Leu Val Asn Gly Leu Ala Leu Gln

100 105 110
 Leu Arg Asn Thr Ser Arg Ser Glu Glu Asp Arg Asn Arg Asp Leu Ala
 115 120 125
 5 Thr Ala Leu Glu Gln Leu Leu Gln Ala Tyr Pro Arg Asp Met Glu Lys
 130 135 140
 Glu Lys Thr Met Leu Val Leu Ala Leu Leu Leu Ala Lys Lys Val Ala
 10 145 150 155 160
 Ser His Thr Pro Ser Leu Leu Arg Asp Val Phe His Thr Thr Val Asn
 165 170 175
 15 Phe Ile Asn Gln Asn Leu Arg Thr Tyr Val Arg Ser Leu Ala Arg Asn
 180 185 190
 Gly Met Asp
 20 195

(2) INFORMATION FOR SEQ ID NO: 156:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

30 Met Ser Leu Ser Leu Val Ser Val Ser Val Gly Pro Ser Thr Leu Ala
 1 5 10 15
 35 Cys Ser Phe Leu Arg Pro Lys Ala Arg Pro Ser Lys Arg Ser Pro Arg
 20 25 30
 Asn Tyr Thr Asp Ser Thr Ser Pro Gly Gly Pro Arg Ala Pro Arg Gly
 35 40 45
 40 Gly Ala Trp Arg Leu Ser Ser Gln Gln Asn Ser Ser Pro Lys Gly Val
 50 55 60
 Ala Val Ala Lys Ala Ser Tyr Arg Pro Val Leu Cys Phe Leu Pro Gly
 65 70 75 80
 45 Pro Trp Ser Ser Xaa Pro Xaa Ala Phe Leu Ile
 85 90

50

(2) INFORMATION FOR SEQ ID NO: 157:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

60 Met Gly Thr Leu Ser Ala Glu Cys Ser Gly Pro Ala Thr Leu Gly Leu
 1 5 10 15

290

Cys Leu Val Val Pro Trp Asn Ser Ser Gly Leu Ser Gln Pro Pro
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

15 Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
 1 5 10 15

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
 20 25 30

20

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
 35 40 45

25 Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
 50 55 60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
 65 70 75 80

30 Gly Asp Leu Pro Asn Gly Arg Val Cys Pro Xaa
 85 90

35 (2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

40

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

45 Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
 1 5 10 15

Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
 20 25 30

50

Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
 35 40 45

Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
 50 55 60

55

Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Trp Asp Trp Ala
 65 70 75 80

Glu Ala Gly Ala Ser Leu Tyr Ser Pro
 85

60

(2) INFORMATION FOR SEQ ID NO: 160:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

10

Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
 1 5 10 15

15

Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
 20 25 30

Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Glu Gln Glu Ser Gln
 35 40 45

20

Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
 50 55 60

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Glu Arg Lys Ile Asn
 65 70 75 80

25

Lys Met Thr Asp Lys Leu Lys Thr His Val Lys Ala Arg Thr Ala Gln
 85 90 95

30

Leu Ala Lys Ile Lys Trp Val Ile Ser Val Ala Phe Tyr Val Leu Gln
 100 105 110

Ala Ala Leu Met Ile Ser Leu Ile Trp Lys Tyr Tyr Ser Val Pro Val
 115 120 125

35

Ala Val Val Pro Ser Lys Trp Ile Thr Pro Leu Asp Arg Leu Val Ala
 130 135 140

Phe Pro Thr Arg Val Ala Gly Gly Val Gly Ile Thr Cys Trp Ile Leu
 145 150 155 160

40

Val Cys Asn Lys Val Val Ala Ile Val Leu His Pro Phe Ser
 165 170

45

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

50

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

55

Met Gly Lys Leu Ile Asn Ile Val Ile Arg Lys Pro Leu Leu Leu Leu
 1 5 10 15

Leu Val Gln Cys Glu Asn Cys Cys Arg Lys Asn Met Leu Tyr Asn Ile
 20 25 30

60

Phe Leu Asn Ile His Asn Ile His Lys Phe Ser Asn His

35

40

45

5 (2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Met Val Ala Ser Thr Leu Val Thr Asn Leu Phe Gly Val Ala Phe Ala
 1 5 10 15

15 Thr Thr Ala Ala Thr Arg Ala
 20

20

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

25 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

30 Met Leu Met Ala Pro Val Val Cys Leu Ser Phe Ser Pro Cys Pro Ala
 1 5 10 15

Asp Thr Ser Leu Thr Gly Asp Gly Leu Lys Ala Gly Leu Glu Arg Gly
 20 25 30

35 Xaa Ala Leu Val Thr Leu Phe Asp Ser Val Thr His Phe Leu Ala His
 35 40 45

Thr Leu Phe Glu Leu Leu Asp Phe Gln Leu Ala Phe Leu Arg Ser Gly
 50 55 60

40

Lys Gln Thr Ala Pro His
 65 70

45

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 amino acids

50 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

55 Met Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln
 1 5 10 15

Val Gly Ala Gly Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu
 20 25 30

60 Ser Lys Pro Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn

293

	35	40	45
	Leu Met Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro		
	50	55	60
5	Asp Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe		
	65	70	75 80
10	Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln Gly		
		85	90 95
	Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr Arg Asn		
		100	105 110
15	Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys Phe Val Gly		
		115	120 125
	Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu		
		130	135 140
20	Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn Asn Gly Ser Leu Ser		
		145	150 155 160
	Tyr Asp His Glu Arg Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Thr		
		165	170 175
25	Ala Ile Val Arg Asn Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr		
		180	185 190
30	Val Lys Arg His Leu Thr Ile Met Met Asp Ile Asp Gly Lys His Glu		
		195	200 205
	Trp Arg Asp Cys Ile Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr		
		210	215 220
35	Tyr Phe Gly Thr Ser Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp		
		225	230 235 240
	Val Ile Ser Leu Lys Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu		
		245	250 255
40	Glu Glu Lys Leu His Arg Asp Val Phe Leu Pro Ser Val Asp Asn Met		
		260	265 270
45	Lys Leu Pro Glu Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala		
		275	280 285
	Leu Phe Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile		
		290	295 300
50	Val Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys		
		305	310 315 320
55	Arg Phe Tyr		

(2) INFORMATION FOR SEQ ID NO: 165:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

	Met	Pro	Ser	Glu	Tyr	Thr	Tyr	Val	Lys	Leu	Arg	Ser	Asp	Cys	Ser	Arg	
	1				5					10					15		
10	Pro	Ser	Leu	Gln	Trp	Tyr	Thr	Arg	Ala	Gln	Ser	Lys	Met	Arg	Arg	Pro	
				20					25					30			
	Ser	Leu	Leu	Leu	Lys	Asp	Ile	Leu	Lys	Cys	Thr	Leu	Leu	Val	Phe	Gly	
				35				40					45				
15	Val	Trp	Ile	Leu	Tyr	Ile	Leu	Lys	Leu	Asn	Tyr	Thr	Thr	Glu	Glu	Cys	
		50					55					60					
	Asp	Met	Lys	Lys	Met	His	Tyr	Val	Asp	Pro	Asp	His	Val	Lys	Arg	Ala	
20		65				70					75					80	
	Gln	Lys	Tyr	Ala	Gln	Gln	Val	Leu	Gln	Lys	Glu	Cys	Arg	Pro	Lys	Phe	
					85					90					95		
25	Ala	Lys	Thr	Ser	Met	Ala	Leu	Leu	Phe	Glu	His	Arg	Tyr	Ser	Val	Asp	
				100					105					110			
	Leu	Leu	Pro	Phe	Val	Gln	Lys	Xaa	Pro	Lys	Asp	Ser	Glu	Ala	Glu	Ser	
			115					120					125				
30	Lys	Tyr	Asp	Pro	Pro	Phe	Gly	Phe	Arg	Lys	Phe	Ser	Ser	Lys	Val	Gln	
		130					135				140						
	Thr	Leu	Leu	Glu	Leu	Leu	Pro	Glu	His	Asp	Leu	Pro	Glu	His	Leu	Lys	
35		145				150					155					160	
	Ala	Lys	Thr	Cys	Arg	Arg	Cys	Val	Val	Ile	Gly	Ser	Gly	Gly	Ile	Leu	
					165					170					175		
40	His	Gly	Leu	Glu	Leu	Gly	His	Thr	Leu	Asn	Gln	Phe	Asp	Val	Val	Ile	
				180					185					190			
	Arg	Leu	Asn	Ser	Ala	Pro	Val	Glu	Gly	Tyr	Ser	Glu	His	Val	Gly	Asn	
			195					200				205					
45	Lys	Thr	Thr	Ile	Arg	Met	Thr	Tyr	Pro	Glu	Gly	Ala	Pro	Leu	Ser	Asp	
		210					215					220					
	Leu	Glu	Tyr	Tyr	Ser	Asn	Asp	Leu	Phe	Val	Ala	Val	Leu	Phe	Lys	Ser	
50		225				230					235					240	
	Val	Asp	Phe	Asn	Trp	Leu	Gln	Ala	Met	Val	Lys	Lys	Glu	Thr	Leu	Pro	
				245					250					255			
55	Phe	Trp	Val	Arg	Leu	Phe	Phe	Trp	Lys	Gln	Val	Ala	Glu	Lys	Ile	Pro	
				260				265					270				
	Leu	Gln	Pro	Lys	His	Phe	Arg	Ile	Leu	Asn	Pro	Val	Ile	Ile	Lys	Glu	
			275					280					285				

60

295

Thr Ala Phe Xaa His Pro Ser Val Leu Arg Ala Ser Val Lys Val Leu
 290 295 300

5 Gly Ala Glu Ile Arg Thr Ser Pro Gln Ser Val Ser Leu Pro Leu Ser
 305 310 315 320

Xaa

10

(2) INFORMATION FOR SEQ ID NO: 166:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

20 Met Thr Leu Asp Val Gln Thr Val Val Val Phe Ala Val Ile Val Val
 1 5 10 15

Leu Leu Leu Val Asn Val Ile Leu Met Phe Phe Leu Gly Thr Arg
 20 25 30

25

(2) INFORMATION FOR SEQ ID NO: 167:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

35 Met Leu Pro Leu Leu Phe Cys Ala Phe Cys Leu His Lys Leu Gly Pro
 1 5 10 15

40 Leu Leu Phe Leu Tyr Asp Val Leu Met Xaa His Glu Ala Val Met Arg
 20 25 30

Thr His Gln Ile Gln Leu Pro Asp Pro Glu Phe Pro Ser Gln Gln Asn
 35 40 45

45 Gln Val Leu Asn Lys Thr Leu Phe Asn Lys Leu Lys Lys Lys Lys Lys
 50 55 60

Lys Lys Lys Xaa Xaa Xaa Lys Lys
 65 70

50

(2) INFORMATION FOR SEQ ID NO: 168:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

60

296

Met Ala Ser Arg Gly Arg Arg Pro Glu His Gly Gly Pro Pro Glu Leu
 1 5 10 15
 5 Phe Tyr Asp Glu Thr Glu Ala Arg Lys Tyr Val Arg Asn Ser Arg Met
 20 25 30
 Ile Asp Ile Gln Thr Arg Met Ala Gly Arg Ala Leu Glu Leu Leu Tyr
 35 40 45
 10 Leu Pro Glu Asn Lys Pro Cys Tyr Leu Leu Asp Ile Gly Cys Gly Thr
 50 55 60
 Gly Leu Ser Gly Ser Tyr Leu Ser Asp Glu Gly His Tyr Trp Val Gly
 65 70 75 80
 15 Leu Asp Ile Ser Pro Ala Met Leu Asp Glu Ala Val Asp Arg Glu Ile
 85 90 95
 20 Glu Gly Asp Leu Leu Leu Gly Asp Met Gly Gln Gly Ile Pro Phe Lys
 100 105 110
 Pro Gly Thr Phe Asp Gly Cys Ile Ser Ile Ser Ala Val Gln Trp Leu
 115 120 125
 25 Cys Asn Ala Asn Lys Lys Ser Glu Asn Pro Ala Lys Arg Leu Tyr Cys
 130 135 140
 Phe Phe Ala Ser Leu Phe Ser Val Leu Val Arg Gly Ser Arg Ala Val
 145 150 155 160
 30 Leu Gln Leu Tyr Pro Glu Asn Ser Glu Gln Leu Glu Leu Ile Thr Thr
 165 170 175
 35 Gln Ala Thr Lys Ala Gly Phe Ser Gly Gly Met Val Val Asp Tyr Pro
 180 185 190
 Asn Ser Ala Lys Ala Lys Lys Phe Tyr Leu Cys Leu Phe Ser Gly Pro
 195 200 205
 40 Ser Thr Phe Ile Pro Glu Gly Leu Ser Glu Asn Gln Asp Glu Val Glu
 210 215 220
 Pro Arg Glu Ser Val Phe Thr Asn Glu Arg Phe Pro Leu Arg Met Ser
 225 230 235 240
 45 Arg Arg Gly Met Val Arg Lys Ser Arg Ala Trp Val Leu Glu Lys Lys
 245 250 255
 50 Glu Arg His Arg Arg Gln Gly Arg Glu Val Arg Pro Asp Thr Gln Tyr
 260 265 270
 Thr Gly Arg Lys Arg Lys Pro Arg Phe Xaa
 275 280

55

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 amino acids

297

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5 Met Leu Gly Lys Thr Lys Phe Gln Ser Tyr Lys Ser Phe Ser Arg Lys
 1 5 10 15

Leu Met Val Cys Pro Ser Thr
 20

10

(2) INFORMATION FOR SEQ ID NO: 170:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

20

Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His Gly
 1 5 10 15

25

Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly Arg
 20 25 30

Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala His
 35 40 45

30

Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val Ala
 50 55 60

Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu Gly
 65 70 75 80

35

Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp Val
 85 90 95

40

Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg His
 100 105 110

Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp Arg
 115 120 125

45

Asp Gly Arg Val Gly Trp Glu Leu Arg Asn Ala Thr Tyr Gly His
 130 135 140

Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr Tyr
 145 150 155 160

50

Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp Gln
 165 170 175

55

Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu His
 180 185 190

Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr Leu
 195 200 205

60

Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu Tyr

[illegible]

25

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

35

Met Cys Trp Leu Arg Ala Trp Xaa Gln Ile Xaa Leu Pro Val Phe Xaa
1 5 10 15

Ser Xaa Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly Phe
20 25 30

40

Ile His Ser Pro Arg Asn Asn Gln Lys Pro Arg Asp Gly Asn Xaa Glu
35 40 45

Glu Cys Ala Val Lys Lys Ser Cys Gln Leu Cys Thr Glu Asp Lys Lys
50 55 60

45

Tyr Met Met Asn Arg
65

50

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

60

Met Trp Leu Phe Ile Leu Leu Ser Leu Ala Leu Ile Ser Asp Ala Met
1 5 10 15

299

Val Met Asp Glu Lys Val Lys Arg Ser Phe Val Leu Asp Thr Ala Ser
 20 25 30

5 Ala Ile Cys Asn Tyr Asn Ala His Tyr Lys Asn His Pro Lys Tyr Trp
 35 40 45

Cys Arg Gly Tyr Phe Arg Asp Tyr Cys Asn Ile Ile Ala Phe Ser Pro
 50 55 60

10 Asn Ser Thr Asn His Val Ala Leu Lys Asp Thr Gly Asn Gln Leu Ile
 65 70 75 80

15 Val Thr Met Ser Cys Leu Asn Lys Glu Asp Thr Gly Trp Tyr Trp Cys
 85 90 95

Gly Ile Gln Arg Asp Phe Ala Arg Asp Asp Met Asp Phe Thr Glu Leu
 100 105 110

20 Ile Val Thr Asp Asp Lys Gly Thr Trp Pro Met Thr Leu Val Trp Glu
 115 120 125

Arg Leu Ser Gly Thr Lys Pro Glu Ala Ala Arg Leu Pro Lys Leu Ser
 130 135 140

25 Ala Arg Leu Thr Ala Pro Gly Arg Pro Phe Ser Ser Phe Ala Tyr Xaa
 145 150 155 160

30

- (2) INFORMATION FOR SEQ ID NO: 173:
- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Met Ala Xaa His Phe Leu Leu Val Ala Leu Gln Ser Val Pro His Cys
 1 5 10 15

45 Pro His Leu Leu Glu Glu Glu His Lys Leu Cys Lys Val Ser His Phe
 20 25 30

Ser Gly Val Thr Leu Val Thr Ser Arg Gln Asp Ser Ser Ser Tyr Val
 35 40 45

50 Pro Val Gln Thr Leu Phe Ile His Leu Gly Pro Trp Ala Trp Asp Leu
 50 55 60

55 Xaa Pro Cys Thr Ala Glu Asp Pro Glu Ala Glu Arg Ser Leu Arg Leu
 65 70 75 80

Cys His Ser His Leu Ala Arg Xaa Asn Val Ser Pro Ser Gln Ala Ala
 85 90 95

60 Glu Gly Xaa Xaa Xaa Arg Gly Cys Gln His Arg Gly Ser Arg Glu Leu

300

100 105 110
 Thr Phe Leu Ser Ala Glu Asn Glu Ala Gly Ile
 115 120

5

(2) INFORMATION FOR SEQ ID NO: 174:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

15

Met Lys Val Gly Ala Arg Ile Arg Val Lys Met Ser Val Asn Lys Ala
 1 5 10 15

20

His Pro Val Val Ser Thr His Trp Arg Trp Pro Ala Glu Trp Pro Gln
 20 25 30

Met Phe Leu His Leu Ala Gln Glu Pro Arg Thr Glu Val Lys Ser Arg
 35 40 45

25

Pro Leu Gly Leu Ala Gly Phe Ile Arg Gln Asp Ser Lys Thr Arg Lys
 50 55 60

Pro Leu Glu Gln Glu Thr Ile Met Ser Ala Ala Asp Thr Ala Leu Trp
 65 70 75 80

30

Pro Tyr Gly His Gly Asn Arg Glu His Gln Glu Asn Glu Leu Gln Lys
 85 90 95

35

Tyr Leu Gln Tyr Lys Asp Met His Leu Leu Asp Ser Gly Gln Ser Leu
 100 105 110

Gly His Thr His Thr Leu Gln Gly Ser His Asn Leu Thr Ala Leu Asn
 115 120 125

40

Ile

45 (2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

50

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Met Ala Tyr His Ser Phe Leu Val Glu Pro Ile Ser Cys His Ala Trp
 1 5 10 15

55

Asn Lys Asp Arg Thr Gln Ile Ala Ile Cys Pro Asn Asn His Glu Val
 20 25 30

60

His Ile Tyr Glu Lys Ser Gly Ala Lys Trp Thr Lys Val His Glu Leu
 35 40 45

Lys Glu His Asn Gly Gln Val Thr Gly Ile Asp Trp Ala Pro Glu Ser
 50 55 60

5 Asn Arg Ile Val Thr Cys Gly Thr Asp Arg Asn Ala Tyr Val Trp Thr
 65 70 75 80

Leu Lys Gly Arg Thr Trp Lys Pro Thr Leu Val Ile Leu Arg Ile Asn
 85 90 95

10 Arg Ala Ala Arg Cys Val Arg Trp Ala Pro Asn Glu Asn Lys Phe Ala
 100 105 110

Val Gly Ser Gly Ser Arg Val Ile Ser Ile Cys Tyr Phe Glu Gln Glu
 115 120 125

15 Asn Asp Trp Trp Val Cys Lys His Ile Lys Lys Pro Ile Arg Ser Thr
 130 135 140

20 Val Leu Ser Leu Asp Trp His Pro Asn Asn Val Leu Leu Ala Ala Gly
 145 150 155 160

Ser Cys Asp Phe Lys Cys Arg Ile Phe Ser Ala Tyr Ile Lys Glu Val
 165 170 175

25 Glu Glu Arg Pro Ala Pro Thr Pro Trp Gly Ser Lys Met Pro Phe Gly
 180 185 190

30 Glu Leu Met Phe Glu Ser Ser Ser Ser Cys Gly Trp Val His Gly Val
 195 200 205

Cys Phe Ser Ala Ser Gly Ser Arg Val Ala Trp Val Ser His Asp Ser
 210 215 220

35 Thr Val Cys Leu Ala Asp Ala Asp Lys Lys Met Ala Val Ala Thr Leu
 225 230 235 240

Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu Thr Phe Ile Thr Asp Asn
 245 250 255

40 Ser Leu Val Ala Ala Gly His Asp Cys Phe Pro Val Leu Phe Thr Tyr
 260 265 270

Asp Ala Ala Ala Gly Met Leu Ser Phe Gly Gly Arg Leu Asp Val Pro
 275 280 285

Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala Arg Glu Arg Phe Gln Asn
 290 295 300

50 Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly Thr Ala Ala Gly Ala Gly
 305 310 315 320

Leu Asp Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser
 325 330 335

55 Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly
 340 345 350

Gly Met Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp
 355 360 365

60

302

Leu Lys Ile Lys
370

5

(2) INFORMATION FOR SEQ ID NO: 176:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

15

Met Trp Ser Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu
1 5 10 15

Leu Leu Ala Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala
20 25 30

20

Leu Glu Tyr Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro
35 40 45

25

Arg Thr Phe Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile
50 55 60

Met Ala Val Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala
65 70 75 80

30

Asp Leu Ser Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu
85 90 95

Tyr Ala Val Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln
100 105 110

35

Pro Tyr Phe Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr
115 120 125

40

Gly Pro Gln Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly
130 135 140

Val Trp Tyr Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn
145 150 155 160

45

Leu Glu Gly Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser
165 170 175

Gly Lys Gln Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp
180 185 190

50

Lys Val Asn Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro
195 200 205

55

Gln Thr Leu Ala Ser Glu Lys Lys
210 215

60

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Met Lys Pro Val Ser Arg Arg Thr Leu Asp Trp Ile Tyr Ser Val Leu
 1 5 10 15

10 Leu Leu Ala Ile Val Leu Ile Ser Trp Gly Cys Ile Ile Tyr Ala Ser
 20 25 30

Met Val Ser Ala Arg Arg Gln Leu Arg Lys Lys Tyr Pro Asp Lys Ile
 35 40 45

15 Phe Gly Thr Asn Glu Asn Leu
 50 55

20

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

30 Met Ala Ala Asn Thr Phe Val Leu Ile Met Gly Ile Pro Thr Ser Ala
 1 5 10 15

Asn Ala Xaa Arg Asp Leu Phe
 20

35

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

45 Met Ser Ile Cys His Arg Gly Thr Gly Ile Ala Leu Ser Ala Gly Val
 1 5 10 15

Ser Leu Phe Gly Met Ser Ala Leu Leu Leu Pro Gly Asn Phe Glu Ser
 20 25 30

50

Tyr Leu Glu Leu Val Lys Ser Leu Cys Leu Gly Pro Ala Leu Ile His
 35 40 45

55

Thr Ala Lys Phe Ala Leu Val Phe Pro Leu Met Tyr His Thr Trp Asn
 50 55 60

Gly Ile Arg His Leu Met Trp Asp Leu Gly Lys Gly Leu Lys Ile Pro
 65 70 75 80

60 Gln Leu Tyr Gln Ser Gly Val Val Val Leu Val Leu Thr Val Leu Ser

304

85 90 95

Ser Met Gly Leu Ala Ala Met
100

5

(2) INFORMATION FOR SEQ ID NO: 180:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

15

Met Thr Lys Ala Ser Ser Leu Trp Pro Leu Lys Thr Thr Cys Gln Ile
1 5 10 15

20

Ser Gly Thr Val Phe Phe Phe Leu Phe Leu Phe Ser Cys Phe Leu Met
20 25 30

Gln Ala Gln Cys Asp Lys Phe Val Gly Trp Asp Phe Phe Phe Phe Leu
35 40 45

25

30

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Met Arg Arg Ala Leu Ile Pro Pro Cys Arg Gly Gly Pro Ser Ala Ser
1 5 10 15

40

Asp Xaa Cys Cys Ser Cys Ser Pro Ser Gly Phe Ser Ala Gly Arg Gly
20 25 30

45

Arg Cys Pro Val Gln Gly Cys Leu Arg Pro His Arg Val Gln Leu Leu
35 40 45

Arg Arg Trp Gly Pro Gly Ser Pro Ala Gly Gln Arg Leu Ser Lys Gly
50 55 60

50

Phe Gln Leu Leu Arg Trp Trp Gly Pro Gly Ser Pro Ala Pro Glu Pro
65 70 75 80

Arg Lys Gly Pro Phe Pro Pro Pro Asp Pro Pro Trp Pro Val Thr Leu
85 90 95

55

60

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

5 Met Leu Glu Thr Thr Lys His Val Gln Ile Ala Cys Met Leu Leu Leu
 10 1 5 10 15
 Thr Cys Gln Ile Phe Leu Pro Ser Ser Leu Ser Pro Ser Phe Ile His
 20 25 30
 15 Ser Leu Thr Asp Ser Phe Ile Pro Leu Lys Lys Leu Tyr Val Cys Phe
 35 40 45
 Val Gln Ser Thr Leu Leu Lys Ala Ala Gly Tyr Lys Ser Ile Ser Glu
 50 55 60
 20 Ala Leu Gly Phe Asp Xaa Leu Leu Cys Ser Ser Ala Arg Phe Val Trp
 65 70 75 80
 25 Ile Cys His Thr Tyr Ser Arg Pro Leu Val Thr Cys Ala Leu His
 85 90 95

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

30 Met Ser Val Ile Gly Gly Leu Leu Leu Val Val Ala Leu Gly Pro Gly
 1 5 10 15
 40 Gly Val Ser Met Asp Glu Lys Lys Lys Glu Trp
 20 25

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

50 Met Ser Gly Gly Leu Ser Phe Leu Leu Leu Val
 1 5 10
 55

(2) INFORMATION FOR SEQ ID NO: 185:

60 (i) SEQUENCE CHARACTERISTICS:

306

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

5

Met Phe Ala Asp Phe Ile Val Val Thr Ala Thr Val Gln Arg Cys Pro
 1 5 10 15

10

Gly Ser Pro Pro Leu Ser Glu Ile Leu Trp Lys Asp Glu Pro Phe Ala
 20 25 30

Ile Ser Ser His Ala Gly Leu Pro Trp Leu Ser Ser Trp Pro Ala Pro
 35 40 45

15

Pro Trp Thr Trp Ser Trp Ile Ser Arg Arg Arg Glu His Gly Arg Gly
 50 55 60

Ser
 65

20

(2) INFORMATION FOR SEQ ID NO: 186:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

30

Met Val Glu Ser Val Met Pro Val Val Val Cys Thr Leu Ser Pro Gly
 1 5 10 15

35

Ile Asp Ser Ser Pro Ser
 20

40

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
 1 5 10 15

50

Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
 20 25 30

Val Val Tyr Tyr Thr Val Thr Pro Ser Tyr Asp Asp Phe Ser Ala
 35 40 45

55

Asp Phe Thr Ile Asp Tyr Ser Ile Phe Glu Ser Glu Asp Arg Leu Asn
 50 55 60

60

Arg Leu Asp Lys Asp Ile Thr Glu Ala Ile Glu Thr Thr Ile Ser Leu
 65 70 75 80

Glu Thr Ala Arg Ala Asp His Pro Lys Pro Val Thr Val Lys Pro Val
 85 90 95
 5 Thr Thr Glu Pro Gln Ser Pro Asp Leu Asn Asp Ala Val Ser Ser Leu
 100 105 110
 Arg Ser Pro Ile Pro Leu Leu Leu Ser Cys Ala Phe Val Gln Val Gly
 115 120 125
 10 Met Tyr Phe Met
 130

15

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

25 Met Pro Cys Gln Pro Gly Gln Val Pro Ser Cys Gln Cys Thr Phe Gly
 1 5 10 15
 Leu Leu Leu Met Leu Pro Ser Leu Pro Ser Pro Ala Ser Gln Pro Arg
 20 25 30
 30 Pro Phe Cys Ser Ser Met Glu Tyr Phe His Gly Cys Ala Ser Pro Ser
 35 40 45
 Gln Ala Ile Ile Gly Gly Phe Pro Phe Ala Ser Val Ala Leu Ala Asp
 50 55 60
 35 Ile Leu Cys Leu Gln
 65

40

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

50 Met Ser Leu Leu Ser Pro Ala Ile Pro Ala Leu Thr Leu Ile Phe Ile
 1 5 10 15
 Leu Met Phe Phe Ser Phe Pro Phe Arg Ala His Thr Val Val Thr Ile
 20 25 30
 55 Val Ala Ser Gly Phe Leu Gly Leu Ser Pro Leu Cys Gly
 35 40 45

60

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Met Ala Phe Gly Leu Gln Met Phe Ile Gln Arg Lys Phe Pro Tyr Pro
 1 5 10 15

Leu Gln Trp Ser Leu Leu Val Ala Val Val Ala Gly Ser Val Val Ser
 20 25 30

Tyr Gly Val Thr Arg Val Glu Ser Glu Lys Cys Asn Asn Leu Trp Leu
 35 40 45

Phe Leu Glu Thr Gly Gln Leu Pro Lys Asp Arg Ser Thr Asp Gln Arg
 50 55 60

Ser
 65

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met Leu Lys
 1 5 10 15

Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser Phe Ile Ser Phe
 20 25 30

Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met Met Ser Ser Phe
 35 40 45

Met Xaa
 50

45

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Leu Leu Asn Val Ala Leu Val Ala Leu Val Leu Leu Gly Ala Tyr
 1 5 10 15

Arg Leu Trp Val Arg Trp Gly Arg Arg Gly Leu Gly Ala Gly Ala Gly
 20 25 30

60

309

Ala Gly Glu Glu Ser Pro Ala Thr Ser Leu Pro Arg Met Lys Lys Arg
 35 40 45

5 Asp Phe Ser Leu Glu Gln Leu Arg Gln Tyr Asp Gly Ser Arg Asn Pro
 50 55 60

Arg Ile Leu Leu Ala Val Asn Gly Lys Val Phe Asp Val Thr Lys Gly
 65 70 75 80

10 Ser Lys Phe Tyr Gly Pro Ala Gly Pro Tyr Gly Ile Phe Ala Gly Arg
 85 90 95

Asp Ala Ser Arg Gly Leu Ala Thr Phe Cys Leu Asp Lys Asp Ala Leu
 100 105 110

15 Arg Asp Glu Tyr Asp Asp Leu Ser Asp Leu Asn Ala Val Gln Met Glu
 115 120 125

Ser Val Arg Glu Trp Glu Met Gln Phe Lys Glu Lys Tyr Asp Tyr Val
 130 135 140

Gly Arg Leu Leu Lys Pro Gly Glu Glu Pro Ser Glu Tyr Thr Asp Glu
 145 150 155 160

25 Glu Asp Thr Lys Asp His Asn Lys Gln Asp
 165 170

30 (2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Met Thr Tyr Phe Ser Gly Leu Leu Val Ile Leu Ala Phe Ala Ala Trp
 1 5 10 15

40 Val Ala Leu Ala Glu Gly Leu Gly Val Ala Val Tyr Ala Ala Ala Val
 20 25 30

Leu Leu Gly Ala Gly Cys Ala Thr Ile Leu Val Thr Ser Leu Ala Met
 35 40 45

Thr Ala Asp Leu Ile Gly Pro His Thr Asn Ser Gly Leu Ser Cys Thr
 50 55 60

50 Ala Pro
 65

55 (2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

5 Met Ala Ala Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu Arg
 1 5 10 15
 Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu
 20 25 30
 10 Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu
 35 40 45
 Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp
 50 55 60
 15 Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys
 65 70 75 80
 Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly
 85 90

20

(2) INFORMATION FOR SEQ ID NO: 195:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

30 Met Arg Gly Ser His Leu Arg Leu Leu Pro Tyr Leu Val Ala Ala Asn
 1 5 10 15
 35 Pro Val Asn Tyr Gly Arg Pro Tyr Arg Leu Ser Cys Val Glu Ala Phe
 20 25 30
 Ala Ala Thr Phe Cys Ile Val Gly Phe Pro Asp Leu Ala Val Ile Leu
 35 40 45
 40 Leu Arg Lys Phe Lys Trp Gly Lys Gly Phe Leu Asp Leu Asn Arg Gln
 50 55 60
 Leu Leu Asp Lys Tyr Ala Ala Cys Gly Ser Pro Glu Glu Val Leu Gln
 65 70 75 80
 45 Ala Glu Gln Glu Phe Leu Ala Asn Ala Lys Glu Ser Pro Gln Glu Glu
 85 90 95
 Glu Ile Asp Pro Phe Asp Val Asp Ser Gly Arg Glu Phe Gly Asn Pro
 100 105 110
 Asn Arg Pro Val Ala Ser Thr Arg Leu Pro Ser Asp Thr Asp Asp Ser
 115 120 125
 55 Asp Ala Ser Glu Asp Pro Gly Pro Xaa Ala Glu Arg Gly Gly Ala Ser
 130 135 140
 Ser Ser Cys Cys Glu Glu Glu Gln Thr Gln Gly Arg Gly Ala Glu Ala
 145 150 155 160

60

Arg Ala Pro Ala Glu Val Trp Lys Gly Ile Lys Lys Arg Gln Arg Asp
 165 170 175

5

10

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Met Ser Asn Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr Gly Ile
 1 5 10 15

20

Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg Ala His Leu
 20 25 30

Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly Asn Thr Val Ile
 35 40 45

25

Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe Gly Ser Asn Asp Asp
 50 55 60

30

Phe Ser Trp Gln Gln Trp
 65 70

35

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Met Thr Leu Leu Ile Ile Phe Leu Pro Phe Xaa Phe Thr Thr Xaa Thr
 1 5 10 15

45

Asn Ser Gly Gly Ser Phe Pro Val Arg
 20 25

50

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Met Lys Gly Glu Leu Leu Pro Phe Leu Phe Leu Thr Val Trp Leu Trp
 1 5 10 15

60

312

Leu Tyr Lys Leu Xaa Phe Gly Glu Ser Pro Arg Tyr Pro Asn Val Ile
 20 25 30
 5 Gly Lys Thr Tyr Phe Phe Phe Trp Thr Asp Gln Ile Ser Arg Glu Ser
 35 40 45
 Arg Phe Leu Glu Arg Leu Ala Phe Ile Val Ser Glu Asn Cys Leu Ile
 50 55 60
 10 Phe Leu Ile His Ala Ile Thr Gly Gln
 65 70

15 (2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu
 1 5 10 15
 25 Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
 20 25 30
 30 His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val
 35 40 45
 Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp
 50 55 60
 35 Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr
 65 70 75 80
 Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala
 85 90 95
 40 Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly
 100 105 110
 45 Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys
 115 120 125
 Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu
 130 135 140
 50 Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn
 145 150 155 160
 Val Asp Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys
 165 170 175
 55 Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg
 180 185 190
 60 Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala
 195 200 205

Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His
 210 215 220
 5 Asp His Trp Lys Ala Leu Val Thr Lys Lys Thr Asn Gly Lys Gly Ile
 225 230 235 240
 Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro
 245 250 255
 10 Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser
 260 265 270
 Ala Cys Thr Val Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys
 15 275 280 285
 Asn
 20
 (2) INFORMATION FOR SEQ ID NO: 200:
 (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 625 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:
 30 Met Glu Ile Pro Gly Ser Leu Cys Lys Lys Val Lys Leu Ser Asn Asn
 1 5 10 15
 Ala Gln Asn Trp Gly Met Gln Arg Ala Thr Asn Val Thr Tyr Gln Ala
 20 25 30
 35 His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly Thr Arg Gly
 35 40 45
 Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser Gly Ala Gly
 40 50 55 60
 Lys Thr Thr Val Ser Met Ala Leu Glu Glu Tyr Leu Val Cys His Gly
 65 70 75 80
 45 Ile Pro Cys Tyr Thr Leu Asp Gly Asp Asn Ile Arg Gln Gly Leu Asn
 85 90 95
 Lys Asn Leu Gly Phe Ser Pro Glu Asp Arg Glu Glu Asn Val Arg Arg
 100 105 110
 50 Ile Ala Glu Val Ala Lys Leu Phe Ala Asp Ala Gly Leu Val Cys Ile
 115 120 125
 Thr Ser Phe Ile Ser Pro Tyr Thr Gln Asp Arg Asn Asn Ala Arg Gln
 130 135 140
 55 Ile His Glu Gly Ala Ser Leu Pro Phe Phe Glu Val Phe Val Asp Ala
 145 150 155 160
 60 Pro Leu His Val Cys Glu Gln Arg Asp Val Lys Gly Leu Tyr Lys Lys

		165		170		175	
	Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr Gly Ile Asp Ser Glu Tyr						
		180		185		190	
5	Glu Lys Pro Glu Ala Pro Glu Leu Val Leu Lys Thr Asp Ser Cys Asp		200		205		
		195					
10	Val Asn Asp Cys Val Gln Gln Val Val Glu Leu Leu Gln Glu Arg Asp		215		220		
		210					
	Ile Val Pro Val Asp Ala Ser Tyr Glu Val Lys Glu Leu Tyr Val Pro		230		235		240
		225					
15	Glu Asn Lys Leu His Leu Ala Lys Thr Asp Ala Glu Thr Leu Pro Ala		245		250		255
	Leu Lys Ile Asn Lys Val Asp Met Gln Trp Val Gln Val Leu Ala Glu		260		265		270
20							
	Gly Trp Ala Thr Pro Leu Asn Gly Phe Met Arg Glu Arg Glu Tyr Leu			280		285	
		275					
25	Gln Cys Leu His Phe Asp Cys Leu Leu Asp Gly Gly Val Ile Asn Leu		295		300		
		290					
	Ser Val Pro Ile Val Leu Thr Ala Thr His Glu Asp Lys Glu Arg Leu		310		315		320
		305					
30	Asp Gly Cys Thr Ala Phe Ala Leu Met Tyr Glu Gly Arg Arg Val Ala		325		330		335
	Ile Leu Arg Asn Pro Glu Phe Phe Glu His Arg Lys Glu Glu Arg Cys		340		345		350
35							
	Ala Arg Gln Trp Gly Thr Thr Cys Lys Asn His Pro Tyr Ile Lys Met			360		365	
		355					
40	Val Met Glu Gln Gly Asp Trp Leu Ile Gly Gly Asp Leu Gln Val Leu			375		380	
		370					
	Asp Arg Val Tyr Trp Asn Asp Gly Leu Asp Gln Tyr Arg Leu Thr Pro		390		395		400
		385					
45	Thr Glu Leu Lys Gln Lys Phe Lys Asp Met Asn Ala Asp Ala Val Phe		405		410		415
	Ala Phe Gln Leu Arg Asn Pro Val His Asn Gly His Ala Leu Leu Met		420		425		430
50							
	Gln Asp Thr His Lys Gln Leu Leu Glu Arg Gly Tyr Arg Arg Pro Val			440		445	
		435					
55	Leu Leu Leu His Pro Leu Gly Gly Trp Thr Lys Asp Asp Asp Val Pro			455		460	
		450					
	Leu Met Trp Arg Met Lys Gln His Ala Ala Val Leu Glu Glu Gly Val		470		475		480
		465					
60	Leu Asn Pro Glu Thr Thr Val Val Ala Ile Phe Pro Ser Pro Met Met						

315

485 490 495
 Tyr Ala Gly Pro Thr Glu Val Gln Trp His Cys Arg Ala Arg Met Val
 500 505 510
 5 Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg Asp Pro Ala Gly Met Pro
 515 520 525
 10 His Pro Glu Thr Gly Lys Asp Leu Tyr Glu Pro Ser His Gly Ala Lys
 530 535 540
 Val Leu Thr Met Ala Pro Gly Leu Ile Thr Leu Glu Ile Val Pro Phe
 545 550 555 560
 15 Arg Val Ala Ala Tyr Asn Lys Lys Lys Lys Arg Met Asp Tyr Tyr Asp
 565 570 575
 Ser Glu His His Glu Asp Phe Glu Phe Ile Ser Gly Thr Arg Met Arg
 580 585 590
 20 Lys Leu Ala Arg Glu Gly Gln Lys Pro Pro Glu Gly Phe Met Ala Pro
 595 600 605
 25 Lys Ala Trp Thr Val Leu Thr Glu Tyr Tyr Lys Ser Leu Glu Lys Ala
 610 615 620
 Xaa
 625

30

(2) INFORMATION FOR SEQ ID NO: 201:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 649 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

40 Met Ser Ala Ser Gln Asp Leu Glu Pro Lys Pro Leu Phe Pro Lys Pro
 1 5 10 15
 Ala Phe Gly Gln Lys Pro Pro Leu Ser Thr Glu Asn Ser His Glu Asp
 20 25 30
 45 Glu Ser Pro Met Lys Asn Val Ser Ser Lys Gly Ser Pro Ala Pro
 35 40 45
 50 Leu Gly Val Arg Ser Lys Ser Gly Pro Leu Lys Pro Ala Arg Glu Asp
 50 55 60
 Ser Glu Asn Lys Asp His Ala Gly Glu Ile Ser Ser Leu Pro Phe Pro
 65 70 75 80
 55 Gly Val Val Leu Lys Pro Ala Ala Ser Arg Gly Gly Pro Gly Leu Ser
 85 90 95
 Lys Asn Gly Glu Glu Lys Lys Glu Asp Arg Lys Ile Asp Ala Ala Lys
 100 105 110

60

316

	Asn Thr Phe Gln Ser Lys Ile Asn Gln Glu Glu Leu Ala Ser Gly Thr	
	115 120 125	
5	Pro Pro Ala Arg Phe Pro Lys Ala Pro Ser Lys Leu Thr Val Gly Gly	
	130 135 140	
	Pro Trp Gly Gln Ser Gln Glu Lys Glu Lys Gly Asp Lys Asn Ser Ala	
	145 150 155 160	
10	Thr Pro Lys Gln Lys Pro Leu Pro Pro Leu Phe Thr Leu Gly Pro Pro	
	165 170 175	
	Pro Pro Lys Pro Asn Arg Pro Pro Asn Val Asp Leu Thr Lys Phe His	
15	180 185 190	
	Lys Thr Ser Ser Gly Asn Ser Thr Ser Lys Gly Gln Thr Ser Tyr Ser	
	195 200 205	
20	Thr Thr Ser Leu Pro Pro Pro Pro Pro Ser His Pro Ala Ser Gln Pro	
	210 215 220	
	Pro Leu Pro Ala Ser His Pro Ser Gln Pro Pro Val Pro Ser Leu Pro	
	225 230 235 240	
25	Pro Arg Asn Ile Lys Pro Pro Phe Asp Leu Lys Ser Pro Val Asn Glu	
	245 250 255	
	Asp Asn Gln Asp Gly Val Thr His Ser Asp Gly Ala Gly Asn Leu Asp	
30	260 265 270	
	Glu Glu Gln Asp Ser Glu Gly Glu Thr Tyr Glu Asp Ile Glu Ala Ser	
	275 280 285	
35	Lys Glu Arg Glu Lys Lys Arg Glu Lys Glu Glu Lys Lys Arg Leu Glu	
	290 295 300	
	Leu Glu Lys Lys*Glu Gln Lys Glu Lys Glu Lys Lys Glu Gln Glu Ile	
	305 310 315 320	
40	Lys Lys Lys Phe Lys Leu Thr Gly Pro Ile Gln Val Ile His Leu Ala	
	325 330 335	
	Lys Ala Cys Cys Asp Val Lys Gly Gly Lys Asn Glu Leu Ser Phe Lys	
45	340 345 350	
	Gln Gly Glu Gln Ile Glu Ile Ile Arg Ile Thr Asp Asn Pro Glu Gly	
	355 360 365	
50	Lys Trp Leu Gly Arg Thr Ala Arg Gly Ser Tyr Gly Tyr Ile Lys Thr	
	370 375 380	
	Thr Ala Val Glu Ile Asp Tyr Asp Ser Leu Lys Leu Lys Lys Asp Ser	
	385 390 395 400	
55	Leu Gly Ala Pro Ser Arg Pro Ile Glu Asp Asp Gln Glu Val Tyr Asp	
	405 410 415	
	Asp Val Ala Glu Gln Asp Asp Ile Ser Ser His Ser Gln Ser Gly Ser	
60	420 425 430	

Gly Gly Ile Phe Pro Pro Pro Pro Asp Asp Asp Ile Tyr Asp Gly Ile
 435 440 445
 5 Glu Glu Glu Asp Ala Asp Asp Gly Ser Thr Leu Gln Val Gln Glu Lys
 450 455 460
 Ser Asn Thr Trp Ser Trp Gly Ile Leu Lys Met Leu Lys Gly Lys Asp
 465 470 475 480
 10 Asp Arg Lys Lys Ser Ile Arg Glu Lys Pro Lys Val Ser Asp Ser Asp
 485 490 495
 Asn Asn Glu Gly Ser Ser Phe Pro Ala Pro Pro Lys Gln Leu Asp Met
 500 505 510
 15 Gly Asp Glu Val Tyr Asp Asp Val Asp Thr Ser Asp Phe Pro Val Ser
 515 520 525
 Ser Ala Glu Met Ser Gln Gly Thr Asn Val Gly Lys Ala Lys Thr Glu
 20 530 535 540
 Glu Lys Asp Leu Lys Lys Leu Lys Lys Gln Xaa Lys Xaa Xaa Lys Asp
 545 550 555 560
 25 Phe Arg Lys Lys Phe Lys Tyr Asp Gly Glu Ile Arg Val Leu Tyr Ser
 565 570 575
 Thr Lys Val Thr Thr Ser Ile Thr Ser Lys Lys Trp Gly Thr Arg Asp
 580 585 590
 30 Leu Gln Val Lys Pro Gly Glu Ser Leu Glu Val Ile Gln Thr Thr Asp
 595 600 605
 Asp Thr Lys Val Leu Cys Arg Asn Glu Glu Gly Lys Tyr Gly Tyr Val
 35 610 615 620
 Leu Arg Ser Tyr Leu Ala Asp Asn Asp Gly Glu Ile Tyr Asp Asp Ile
 625 630 635 640
 40 Ala Asp Gly Cys Ile Tyr Asp Asn Asp
 645

45 (2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Met Ala Trp Pro Ser Arg Ser Lys Met Phe Thr Leu Leu Pro Val Leu
 1 5 10 15
 55 Cys Tyr Leu Trp Ser Leu Trp Leu Pro Gln Phe Ser Trp Ile Gln Glu
 20 25 30
 60 Leu Lys Ala Val Leu Arg Asp Asp Gly Leu Ile Ser Ala Val Ala Trp
 35 40 45

Asn Ala Glu Phe Gln Thr Cys
50 55

5

(2) INFORMATION FOR SEQ ID NO: 203:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

15

Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu Ala Lys
1 5 10 15

Lys Asp Glu Pro Lys Ser Gly Glu Glu Ala Leu Ile Ile Pro Pro Asp
20 25 30

20

Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro Val Gly
35 40 45

25

Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala Phe Met
50 55 60

Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr Phe Ala
65 70 75 80

30

Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile Lys Asp
85 90 95

Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala Leu Tyr
100 105 110

35

Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu Val Glu
115 120 125

40

Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro Ala Asn
130 135 140

Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp Leu Asn
145 150 155 160

45

Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val Met Pro
165 170 175

Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly Thr Tyr
180 185 190

50

Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr Asp Arg
195 200 205

55

Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu Cys His
210 215 220

Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys Gly Ile
225 230 235 240

60

Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe Glu Asn

319

245 250 255
 Lys Phe Ala Val Glu Thr Leu Ile Cys Ser Xaa
 260 265

5

(2) INFORMATION FOR SEQ ID NO: 204:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

15

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 1 5 10 15

20

Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
 20 25 30

Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp
 35 40 45

25

His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Thr Phe Asp Gln Leu
 50 55 60

Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
 65 70 75 80

30

Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys Asp Trp
 85 90 95

35

Ile Lys Phe Ala Gln Lys Arg Trp Ile Tyr Glu Asp Val Glu Arg Gln
 100 105 110

Trp Lys Gly His Asp Leu Asn Glu Asp Gly Leu Val Ser Trp Glu Glu
 115 120 125

40

Tyr Lys Asn Ala Thr Tyr Gly Tyr Val Leu Asp Asp Pro Asp Pro Asp
 130 135 140

Asp Gly Phe Asn Tyr Lys Gln Met Met Val Arg Asp Glu Arg Arg Phe
 145 150 155 160

45

Lys Met Ala Asp Lys Asp Gly Asp Leu Ile Ala Thr Lys Glu Glu Phe
 165 170 175

50

Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
 180 185 190

Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
 195 200 205

55

Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
 210 215 220

Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
 225 230 235 240

60

320

	Arg	Asp	Lys	Asn	Arg	Asp	Gly	Lys	Met	Asp	Lys	Glu	Glu	Thr	Lys	Asp	
					245					250						255	
5	Trp	Ile	Leu	Pro	Ser	Asp	Tyr	Asp	His	Ala	Glu	Ala	Glu	Ala	Arg	His	
				260					265						270		
	Leu	Val	Tyr	Glu	Ser	Asp	Gln	Asn	Lys	Asp	Gly	Lys	Leu	Thr	Lys	Glu	
			275					280					285				
10	Glu	Ile	Val	Asp	Lys	Tyr	Asp	Leu	Phe	Val	Gly	Ser	Gln	Ala	Thr	Asp	
		290					295					300					
	Phe	Gly	Glu	Ala	Leu	Val	Arg	His	Asp	Glu	Phe						
	305					310					315						

(2) INFORMATION FOR SEQ ID NO: 205:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

25	Met	Phe	Asp	Ala	Val	Leu	Ile	Leu	Leu	Leu	Ile	Pro	Leu	Lys	Asp	Lys	
	1				5					10					15		
30	Leu	Val	Asp	Pro	Ile	Leu	Arg	Arg	His	Gly	Leu	Leu	Pro	Ser	Ser	Leu	
				20					25					30			
	Lys	Arg	Ile	Ala	Val	Gly	Met	Phe	Phe	Val	Met	Cys	Ser	Ala	Phe	Ala	
			35					40					45				
35	Ala	Gly	Ile	Leu	Glu	Ser	Lys	Arg	Leu	Asn	Leu	Val	Lys	Glu	Lys	Thr	
	50						55					60					
	Ile	Asn	Gln	Thr	Ile	Gly	Asn	Val	Val	Tyr	His	Ala	Ala	Asp	Leu	Ser	
	65					70					75					80	
40	Leu	Trp	Trp	Gln	Val	Pro	Gln	Tyr	Leu	Leu	Ile	Gly	Ile	Ser	Glu	Ile	
					85					90					95		
	Phe	Ala	Ser	Ile	Ala	Gly	Leu	Glu	Phe	Ala	Tyr	Ser	Ala	Ala	Pro	Lys	
45				100					105					110			
	Ser	Met	Gln	Ser	Ala	Ile	Met	Gly	Leu	Phe	Phe	Phe	Phe	Ser	Gly	Val	
			115					120					125				
50	Gly	Ser	Phe	Val	Gly	Ser	Gly	Leu	Leu	Ala	Leu	Val	Ser	Ile	Lys	Ala	
	130						135					140					
	Ile	Gly	Trp	Met	Ser	Ser	His	Thr	Asp	Phe	Gly	Asn	Ile	Asn	Gly	Cys	
	145					150					155					160	
55	Tyr	Leu	Asn	Tyr	Tyr	Phe	Phe	Leu	Leu	Ala	Ala	Ile	Gln	Gly	Ala	Thr	
					165					170					175		
	Leu	Leu	Leu	Phe	Leu	Ile	Ile	Ser	Val	Lys	Tyr	Asp	His	His	Arg	Asp	
60				180					185					190			

321

His Gln Arg Ser Arg Ala Asn Gly Val Pro Thr Ser Arg Arg Ala
 195 200 205

5

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

15 Met Arg Ser Arg Ile Arg Glu Phe Asp Ser Ser Thr Leu Asn Glu Ser
 1 5 10 15
 Val Arg Asn Thr Ile Met Arg Asp Leu Lys Ala Val Gly Lys Lys Phe
 20 20 25 30
 Met His Val Leu Tyr Pro Arg Lys Ser Asn Thr Leu Leu Arg Asp Trp
 35 40 45
 Asp Leu Trp Gly Pro Leu Ile Leu Cys Val Thr Leu Ala Leu Met Leu
 25 50 55 60
 Gln Arg Asp Ser Ala Asp Ser Glu Lys Asp Gly Gly Pro Gln Phe Ala
 65 70 75 80
 30 Glu Val Phe Val Ile Val Trp Phe Gly Ala Val Thr Ile Thr Leu Asn
 85 90 95
 Ser Lys Leu Leu Gly Gly Asn Ile Ser Phe Phe Gln Ser Leu Cys Val
 100 105 110
 35 Leu Gly Tyr Cys Ile Leu Pro Leu Thr Val Ala Met Leu Ile Cys Arg
 115 120 125
 Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn Phe Met Val Arg Leu
 40 130 135 140
 Phe Val Val Ile Val Met Phe Ala Trp Ser Ile Val Ala Ser Thr Ala
 145 150 155 160
 45 Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg Ala Leu Ala Val Tyr
 165 170 175
 Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp Met Ile Leu Thr Phe
 180 185 190
 50 Thr Pro Gln Xaa
 195

55

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid

60

322

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

5	Met	Ala	Lys	Asp	Gln	Ala	Val	Glu	Asn	Ile	Leu	Val	Ser	Pro	Val	Val	1	5	10	15
	Val	Ala	Ser	Ser	Leu	Gly	Leu	Val	Ser	Leu	Gly	Gly	Lys	Ala	Thr	Thr	20	25	30	
10	Ala	Ser	Gln	Ala	Lys	Ala	Val	Leu	Ser	Ala	Glu	Gln	Leu	Arg	Asp	Glu	35	40	45	
	Glu	Val	His	Ala	Gly	Leu	Gly	Glu	Leu	Leu	Arg	Ser	Leu	Ser	Asn	Ser	50	55	60	
15	Thr	Ala	Arg	Asn	Val	Thr	Trp	Lys	Leu	Gly	Ser	Arg	Leu	Tyr	Gly	Pro	65	70	75	80
	Ser	Ser	Val	Ser	Phe	Ala	Asp	Asp	Phe	Val	Arg	Ser	Ser	Lys	Gln	His	85	90	95	
20	Tyr	Asn	Cys	Glu	His	Ser	Lys	Ile	Asn	Phe	Arg	Asp	Lys	Arg	Ser	Ala	100	105	110	
25	Leu	Gln	Ser	Ile	Asn	Glu	Trp	Ala	Ala	Gln	Thr	Thr	Asp	Gly	Lys	Leu	115	120	125	
	Pro	Glu	Val	Thr	Lys	Asp	Val	Glu	Arg	Thr	Asp	Gly	Ala	Leu	Leu	Val	130	135	140	
30	Asn	Ala	Met	Phe	Phe	Lys	Pro	His	Trp	Asp	Glu	Lys	Phe	His	His	Lys	145	150	155	160
	Met	Val	Asp	Asn	Arg	Gly	Phe	Met	Val	Thr	Arg	Ser	Tyr	Thr	Val	Gly	165	170	175	
35	Val	Met	Met	Met	His	Arg	Thr	Gly	Leu	Tyr	Asn	Tyr	Tyr	Asp	Asp	Glu	180	185	190	
40	Lys	Glu	Lys	Leu	Gln	Ile	Val	Glu	Met	Pro	Leu	Ala	His	Lys	Leu	Ser	195	200	205	
	Ser	Leu	Ile	Ile	Leu	Met	Pro	His	His	Val	Glu	Pro	Leu	Glu	Arg	Leu	210	215	220	
45	Glu	Lys	Leu	Leu	Thr	Lys	Glu	Gln	Leu	Lys	Ile	Trp	Met	Gly	Lys	Met	225	230	235	240
	Gln	Lys	Lys	Ala	Val	Ala	Ile	Ser	Leu	Pro	Lys	Gly	Val	Val	Glu	Val	245	250	255	
50	Thr	His	Asp	Leu	Gln	Lys	His	Leu	Ala	Gly	Leu	Gly	Leu	Thr	Glu	Ala	260	265	270	
55	Ile	Asp	Lys	Asn	Lys	Ala	Asp	Leu	Ser	Arg	Met	Ser	Gly	Lys	Lys	Asp	275	280	285	
	Leu	Tyr	Leu	Ala	Ser	Val	Phe	His	Ala	Thr	Ala	Phe	Glu	Leu	Asp	Thr	290	295	300	
60																				

323

Asp Gly Asn Pro Leu Thr Arg Ile Thr Gly Gly Gly Val Arg Thr Gln
 305 310 315 320

5. Val Phe Tyr Ala Asp His Pro Phe Ile Ser Xaa
 325 330

10 (2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

Met Cys Met Gln Leu Phe Gly Phe Leu Ala Phe Met Ile Phe Met Cys
 1 5 10 15
 20 Trp Val Gly Asp Val Tyr Pro Val Tyr Gln Pro Val Gly Pro Lys Gln
 20 25 30
 Tyr Pro Tyr Asn Asn Leu Tyr Leu Glu Arg Gly Gly Asp Pro Ser Lys
 35 40 45
 25 Glu Pro Glu Arg Val Val His Tyr Glu Ile
 50 55

30 (2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

Met Asp Ala Leu Val Glu Asp Asp Ile Cys Ile Leu Asn His Glu Lys
 40 1 5 10 15
 Ala His Lys Arg Asp Thr Val Thr Pro Val Ser Ile Tyr Ser Gly Asp
 20 25 30
 45 Glu Ser Val Ala Ser His Phe Ala Leu Val Thr Ala Tyr Glu Asp Ile
 35 40 45
 Lys Lys Arg Leu Lys Asp Ser Glu Lys Glu Asn Ser Leu Leu Lys Lys
 50 55 60
 50 Arg Ile Arg Phe Leu Glu Glu Lys Leu Ile Ala Arg Phe Glu Glu Glu
 65 70 75 80
 Thr Ser Ser Val Gly Arg Glu Gln Val Asn Lys Ala Tyr His Ala Tyr
 55 85 90 95
 Arg Glu Val Cys Ile Asp Arg Asp Asn Leu Lys Ser Lys Leu Asp Lys
 100 105 110
 60 Met Asn Lys Asp Asn Ser Glu Ser Leu Lys Val Leu Asn Glu Gln Leu

324

115 120 125
 Gln Ser Lys Glu Val Glu Leu Leu Gln Leu Arg Thr Glu Val Glu Thr
 130 135 140
 5 Gln Gln Val Met Arg Asn Leu Asn Pro Pro Ser Ser Asn Trp Glu Val
 145 150 155 160
 10 Glu Lys Leu Ser Cys Asp Leu Lys Ile His Gly Leu Glu Gln Glu Leu
 165 170 175
 Glu Leu Met Arg Lys Glu Cys Ser Asp Leu Lys Ile Glu Leu Gln Lys
 180 185 190
 15 Ala Lys Gln Thr Asp Pro Tyr Gln Glu Asp Asn Leu Lys Ser Arg Asp
 195 200 205
 20 Leu Gln Lys Leu Ser Ile Ser Ser Asp Asn Met Gln His Ala Tyr Trp
 210 215 220
 Glu Leu Lys Arg Glu Met Ser Asn Leu His Leu Val Thr Gln Val Gln
 225 230 235 240
 25 Ala Glu Leu Leu Arg Lys Leu Lys Thr Ser Thr Ala Ile Lys Lys Ala
 245 250 255
 Cys Ala Pro Val Gly Cys Ser Glu Asp Leu Gly Arg Asp Ser Thr Lys
 260 265 270
 30 Leu His Leu Met Asn Phe Thr Ala Thr Tyr Thr Arg His Pro Pro Leu
 275 280 285
 35 Leu Pro Asn Gly Lys Ala Leu Cys His Thr Thr Ser Ser Pro Leu Pro
 290 295 300
 Gly Asp Val Lys Val Leu Ser Glu Lys Ala Ile Leu Gln Ser Trp Thr
 305 310 315 320
 40 Asp Asn Glu Arg Ser Ile Pro Asn Asp Gly Thr Cys Phe Gln Glu His
 325 330 335
 Ser Ser Tyr Gly Arg Asn Ser Leu Glu Asp Asn Ser Trp Val Phe Pro
 340 345 350
 45 Ser Pro Pro Lys Ser Ser Glu Thr Ala Phe Gly Glu Thr Lys Thr Lys
 355 360 365
 50 Thr Leu Pro Leu Pro Asn Leu Pro Pro Leu His Tyr Leu Asp Gln His
 370 375 380
 Asn Gln Asn Cys Leu Tyr Lys Asn
 385 390

55

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

60

325

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

5 Met His His His Thr Gln Leu Met Phe Ile Tyr Leu Phe Ile Tyr Leu
 1 5 10 15
 Phe Ile Leu Gly Val Phe Phe Phe Phe Xaa
 20 25

10

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

20 Met Asn Cys Ile Leu Leu Leu Tyr Leu Leu Ile Pro Thr Ile Ser Ile
 1 5 10 15
 Ser Val Val Pro Tyr Val Ala Leu Asn Ile Lys Tyr Ile Lys Glu Cys
 20 25 30
 25 Thr Glu Asn Ser Phe Tyr Xaa
 35

30

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

40 Met Leu Leu His Leu Thr Ala Ala Phe Leu Gln Arg Ala Gln Phe Ser
 1 5 10 15
 Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
 20 25 30
 45 Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
 35 40 45
 Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
 50 55 60
 50 Arg Val Leu Phe Ile Tyr Xaa
 65 70

55

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid

326

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

5. Met Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe
 1 5 10 15
 Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile
 20 25 30
 10 Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe
 35 40 45
 Ser Thr Tyr Phe Pro Ala Phe Met Asn Ser Leu Ser Arg Ser Lys Arg
 50 55 60
 15 Thr Pro Ala Gly Ser Glu Ser Arg Cys Arg Thr Gln Arg Asn Asn His
 65 70 75 80
 Leu Leu Xaa

20

(2) INFORMATION FOR SEQ ID NO: 214:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Met Ser Lys Arg Ser Ala Ser Phe Ile Leu Leu Pro Leu Leu Phe Leu
 1 5 10 15
 35 Lys Gly Ser Phe Ala Lys Leu Asn Ala Arg Ile Ser Asp Cys Leu Glu
 20 25 30
 Glu Arg Tyr Cys His Asn Leu Trp Met Val Phe Gln Gly Cys Val Ile
 35 40 45
 40 Thr Glu Leu His Leu Ser Arg Met Ser Lys Thr Leu Ser Ser Leu Cys
 50 55 60
 Tyr Asp Phe Val Ile Asn Val Tyr Ile Phe Phe Lys Phe Leu Asp Ile
 45 65 70 75 80
 Thr

50

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

60 Met Cys Ser Leu Phe Glu Ser Arg Phe Phe Cys Phe Val Leu Phe Ser

327

1 5 10 15

Glu Lys Ile Ile Gln Leu Cys Ala Ser Ile Ala Phe Leu Cys Phe Val
20 25 30

5

Lys His Val Pro Trp Pro Lys Trp Lys Arg Lys Cys Leu Ile Asn Ala
35 40 45

10

Phe

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

	Met	Thr	Leu	Arg	Pro	Ser	Leu	Leu	Pro	Leu	His	Leu	Leu	Leu	Leu	
	1				5					10					15	
25	Leu	Leu	Ser	Ala	Ala	Val	Cys	Arg	Ala	Glu	Ala	Gly	Leu	Glu	Thr	Glu
				20					25					30		
	Ser	Pro	Val	Arg	Thr	Leu	Gln	Val	Glu	Thr	Leu	Val	Glu	Pro	Pro	Glu
			35				40						45			
30	Pro	Cys	Ala	Glu	Pro	Ala	Ala	Phe	Gly	Asp	Thr	Leu	His	Ile	His	Tyr
		50					55					60				
	Thr	Gly	Ser	Leu	Val	Asp	Gly	Arg	Ile	Ile	Asp	Thr	Ser	Leu	Thr	Arg
35	65					70					75					80
	Asp	Pro	Leu	Val	Ile	Glu	Leu	Gly	Gln	Lys	Gln	Val	Ile	Pro	Gly	Leu
				85					90						95	
40	Glu	Gln	Ser	Leu	Leu	Asp	Met	Cys	Val	Gly	Glu	Lys	Arg	Arg	Ala	Ile
				100					105					110		
	Ile	Pro	Ser	His	Leu	Ala	Tyr	Gly	Lys	Arg	Gly	Phe	Pro	Pro	Ser	Val
			115					120					125			
45	Pro	Ala	Asp	Ala	Val	Val	Gln	Tyr	Asp	Val	Glu	Leu	Ile	Ala	Leu	Ile
		130					135					140				
	Arg	Ala	Asn	Tyr	Trp	Leu	Lys	Leu	Val	Lys	Gly	Ile	Leu	Pro	Leu	Val
50	145					150					155					160
	Gly	Met	Ala	Met	Val	Pro	Pro	Ser	Trp	Ala	Ser	Leu	Gly	Ile	Thr	Tyr
				165						170					175	
55	Thr	Glu	Arg	Pro	Ile	Asp	Pro	Lys	Ser	Pro	Lys	Arg	Ser	Ser	Arg	Lys
				180					185					190		
	Arg	Asn	Glu	Thr	Arg	Ala	Lys	Arg	Asn	Asn	Lys					
			195					200								

(2) INFORMATION FOR SEQ ID NO: 217:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

10

Met Lys Thr Leu Met Thr Ile Cys Pro Gly Thr Val Leu Leu Val Phe
1 5 10 15

15

Ser Ile Ser Leu Trp Ile Ile Ala Ala Trp Thr Val Arg Val Cys Glu
20 25 30

Ser Pro Glu Ser Pro Ala Gln Pro Ser Gly Ser Ser Leu Pro Ala Trp
35 40 45

20

Tyr His Asp Gln Gln Asp Val Thr Ser Asn Phe Leu Gly Ala Met Trp
50 55 60

Leu Ile Ser Ile Thr Phe Leu Ser Ile Gly Tyr Gly Asp Met Val Pro
65 70 75 80

25

His Thr Tyr Cys Gly Lys Gly Val Cys Leu Leu Thr Gly Ile Met Gly
85 90 95

Ala Gly Cys Thr Ala Leu Val Val Ala Val Val Ala Arg Lys Leu Glu
100 105 110

30

Leu Thr Lys Ala Glu Lys His Val His Xaa Phe Met Met Asp Thr Gln
115 120 125

35

Leu Thr Lys Arg Ile Lys Asn Xaa Ala Ala Asn Val Leu Xaa Glu Thr
130 135 140

Trp Leu Ile Tyr Lys His Thr Lys Leu Leu Lys Lys Ile Asp His Ala
145 150 155 160

40

Lys Val Arg Asn Thr Arg Gly Ser Ser Ser Lys Tyr Pro Pro Val Glu
165 170 175

Glu Arg Gln Asp Gly Thr Glu Glu Ala Glu
180 185

45

(2) INFORMATION FOR SEQ ID NO: 218:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
1 5 10 15

60

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro

329

20 25 30

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
35 40 45

5 Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
50 55 60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
10 65 70 75 80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
85 90

15

(2) INFORMATION FOR SEQ ID NO: 219:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

25 Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
1 5 10 15

Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
20 25 30

30 Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Glu Gln Glu Ser Gln
35 40 45

Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
35 50 55 60

Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Glu Arg Lys Ile Asn
65 70 75 80

40 Lys Met Thr Asp Lys Leu Lys Thr His Val Lys Ala Arg Thr Ala Gln
85 90 95

Leu Ala Lys Ile Lys Trp Val Ile Ser Val Ala Phe Tyr Val Leu Gln
100 105 110

45 Ala Ala Leu Met Ile Ser Leu Ile Trp Lys Tyr Tyr Ser Val Pro Val
115 120 125

Ala Val Val Pro Ser Lys Trp Ile Thr Leu Xaa
50 130 135

55 (2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

330

Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
 1 5 10 15
 5 Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Leu Pro Ser Phe Ser
 20 25 30
 Ser Phe Met Ser Arg Val Leu Gln Lys Asp Ala Asp Arg Ser His Arg
 35 40 45
 10

15

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:
 20

Met Thr Ala Pro Leu Pro Pro Leu Ser Gly Leu Ala Leu Phe Leu Ile
 1 5 10 15
 Val Phe Phe Ser Leu Gly Val Phe Cys Ile Cys His Ser His Trp Tyr
 20 25 30
 30 His Thr Leu Gln Gln Met Ala Gly Thr Glu Pro Lys Ala Leu Leu Leu
 35 40 45
 Ser Pro Pro Ala Ala Thr Thr Phe Val Thr Val Thr His Glu Val Trp
 50 55 60
 35 Lys Glu Gln Ala Leu Ala
 65 70

40

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:
 45

Met Thr Cys Ser Val Ala Leu Leu Leu Ile Leu Gly Leu Arg Cys Ser
 1 5 10 15
 Gly Val Arg Pro Gly Leu Val Gly Glu Gly His Asn Pro Ser Leu Leu
 20 25 30
 55 Val Cys Leu Leu Leu Lys Asp Ser Arg Thr Asn Gln Gly Ser Cys Pro
 35 40 45
 Gly Gly Pro Trp Ser Glu Arg Asp Ile Glu Ser Val Thr Ser Asp Asn
 50 55 60
 60

Cys Glu Ala Thr Leu Gly Tyr Arg Asn His Ser Leu Pro Ser Asn Tyr
 65 70 75 80

Tyr Asn Ser

5

(2) INFORMATION FOR SEQ ID NO: 223:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Met Leu Thr Arg Ser Leu Lys Thr Leu Pro Ser Ala Cys Thr Ala Phe
 1 5 10 15

20

Leu Leu Leu Phe Phe Leu Phe Ser Ser Gly Asp Pro Glu Leu Ser Cys
 20 25 30

Ser Cys Thr Leu Arg Thr Gln Ser Ser Trp Ser
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 224:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

35

Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His Gly
 1 5 10 15

40

Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly Arg
 20 25 30

Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala His
 35 40 45

45

Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val Ala
 50 55 60

50

Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu Gly
 65 70 75 80

Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp Val
 85 90 95

55

Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg His
 100 105 110

Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp Arg
 115 120 125

60

Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Xaa Thr Tyr Gly His

332

130 135 140

Xaa Xaa Pro Xaa Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr Tyr
 145 150 155 160

5 Lys Lys Met Leu Xaa Arg Asp Glu Arg Arg Phe Arg Val Ala Asp Gln
 165 170 175

Asp Gly Asp Ser Met Ala Thr Arg
 10 180

15 (2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Met Trp Leu Phe Ile Leu Leu Ser Leu Ala Leu Ile Ser Asp Ala Met
 1 5 10 15

25 Val Met Asp Glu Lys Val Lys Arg Ser Leu Cys Trp Thr Arg Leu Leu
 20 25 30

Pro Ser Ala Thr Thr Met Pro Xaa Thr Arg Ile Thr Pro Asn Thr Gly
 35 40 45

30 Ala Glu Xaa Ile Ser Val Xaa Thr Ala Thr Ser Ser Pro Ser Pro Leu
 50 55 60

Thr Ala Pro Ile Met Trp Pro
 35 65 70

40 (2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Met His Val Phe Val Leu Glu Ile Phe Leu
 1 5 10

50

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

60 Met Ala Val Ala Thr Leu Ala Ser Glu Thr Leu Pro Leu Leu Ala Leu

333

1 5 10 15
 Thr Phe Ile Thr Asp Asn Ser Leu Val Ala Ala Gly His Asp Cys Phe
 20 25 30
 5 Pro Val Leu Phe Thr Tyr Asp Ala Ala Ala Gly Met Leu Ser Phe Gly
 35 40 45
 10 Gly Arg Leu Asp Val Pro Lys Gln Ser Ser Gln Arg Gly Leu Thr Ala
 50 55 60
 Arg Glu Arg Phe Gln Asn Leu Asp Lys Lys Ala Ser Ser Glu Gly Gly
 65 70 75 80
 15 Thr Ala Ala Gly Ala Gly Leu Asp Ser Leu His Lys Asn Ser Val Ser
 85 90 95
 Gln Ile Ser Val Leu Ser Gly Gly Lys Ala Lys Cys Ser Gln Phe Cys
 100 105 110
 20 Thr Thr Gly Met Asp Gly Gly Met Ser Ile Trp Asp Val Lys Ser Leu
 115 120 125
 25 Glu Ser Ala Leu Lys Asp Leu Lys Ile Lys
 130 135

30 (2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Leu Gly Ser Leu Ser Thr Ala Pro Ser Ser Ala Leu Pro Thr Leu Gly
 1 5 10 15
 40 Ala Arg Arg Thr Arg Ser Lys
 20

45 (2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Met Thr Tyr Phe Ser Gly Leu Leu Val Ile Leu Ala Phe Ala Ala Trp
 1 5 10 15
 55 Val Ala Leu Ala Glu Gly Leu Gly Val Ala Val Tyr Ala Ala Ala Val
 20 25 30
 60 Leu Leu Gly Ala Gly Cys Ala Thr Ile Leu Val Thr Ser Leu Ala Met
 35 40 45

334

Thr Ala Asp Leu Ile Gly Pro His Thr Asn Ser Gly Ala Phe Val Tyr
 50 55 60
 5 Gly Ser Met Ser Phe Leu Asp Lys Val Ala Asn Gly Leu Ala Val Met
 65 70 75 80
 Ala Ile Gln Ser Leu His Pro Cys Pro Ser Glu Leu Cys Cys Arg Ala
 85 90 95
 10 Cys Val Ser Phe Tyr His Trp Ala Met Val Ala Val Thr Gly Gly Val
 100 105 110
 Gly Val Ala Ala Ala Leu Cys Leu Cys Ser Leu Leu Leu Trp Pro Thr
 115 120 125
 15 Arg Leu Arg Arg Xaa
 130

20

(2) INFORMATION FOR SEQ ID NO: 230:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

30 Gly Lys Pro Thr Gly Lys Ser Leu Pro Leu Met Trp Met Ile Leu Met
 1 5 10 15
 Gln Pro Ile Ile Met Ile Ser Met Met Ser Asn Gly
 20 25
 35

(2) INFORMATION FOR SEQ ID NO: 231:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

45 Met Gln Gly Lys Phe Met Lys Val Gln Val Tyr Arg Phe Leu Lys Tyr
 1 5 10 15
 50 Leu Leu Met Leu Leu Cys Met Phe Val Asn Arg Gly Met Ser Lys Asp
 20 25 30
 Ser Thr Lys Lys Pro Gly Gln Glu Lys Leu Lys Val Ser Leu Gly Ser
 35 40 45
 55 Ile Leu Asn Met Lys Ser Gln Arg Pro Leu Ser Trp Cys
 50 55 60

60 (2) INFORMATION FOR SEQ ID NO: 232:

335

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Met Met Glu Arg Ser Met Met Ile Leu Leu Met Ala Ala Ser Met Thr
1 5 10 15

Met Thr Ser Thr Gln Leu Trp Ser Phe Cys Cys Val His
20 25

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Met Trp Tyr Gln Leu Ala Lys Glu Glu Pro Gly Val Gly Ala Cys Ala
1 5 10 15

Leu Asp

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Leu Xaa
.1

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Met Leu Ile Cys Arg Leu Val Leu Leu Ala Asp Pro Gly Pro Val Asn
1 5 10 15

Phe Met Val Arg Leu Phe Val Val Ile Val Met Phe Ala Trp Ser Ile
20 25 30

Val Ala Ser Thr Ala Phe Leu Ala Asp Ser Gln Pro Pro Asn Arg Arg
35 40 45

336

Ala Leu Ala Val Tyr Pro Val Phe Leu Phe Tyr Phe Val Ile Ser Trp
 50 55 60

5 Met Ile Leu Thr Phe Thr Pro Gln
 65 70

10 (2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15

20

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
 20 25 30

25

Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Xaa Pro
 35 40 45

Ala Trp Pro Ser Ala Cys Thr Arg Pro Trp Pro Arg Thr Arg Gln Trp
 50 55 60

30

Arg Thr Ser Trp Cys His Pro Trp Trp Trp Pro Arg Arg Trp Gly Ser
 65 70 75 80

Cys Arg Trp Ala Ala Arg Arg Pro Arg Arg Arg Pro Arg Gln Cys
 85 90 95

35

40

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15

50

Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
 20 25 30

55

Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Lys Arg
 35 40 45

Pro Gly Leu Gln Leu Val Pro Gly His Gly Gln Gly Pro Gly Ser Gly
 50 55 60

60

337

Glu His Pro Gly Val Thr Arg Gly Gly Gly Leu Val Ala Gly Ala Arg
 65 70 75 80
 Val Ala Gly Arg Gln Gly Asp His Gly Val Ala Gly Gln Gly Ser Ala
 5 85 90 95
 Glu Arg Arg Ala Ala Ala Arg Arg Gly Gly Ala Arg Arg Pro Gly Arg
 100 105 110
 10 Ala Ala Ala Leu Thr Gln Gln Leu His Gly Ala Gln Arg Asp Leu Glu
 115 120 125
 Ala Gly Gln Pro Thr Val Arg Thr Gln Leu Ser Glu Leu Arg Xaa
 130 135 140
 15

(2) INFORMATION FOR SEQ ID NO: 238:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

25 Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1 5 10 15
 30 Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
 20 25 30
 Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Xaa Arg
 35 40 45
 35 Pro Gly Leu Gln Leu Val Pro Gly His Gly Gln Gly Pro Gly Ser Gly
 50 55 60
 Glu His Pro Gly Val Thr Arg Gly Gly Gly Leu Val Ala Gly Ala Arg
 65 70 75 80
 40 Val Ala Gly Arg Gln Gly Asp His Gly Val Ala Gly Gln Gly Ser Ala
 85 90 95
 Glu Arg Arg Ala Ala Ala Arg Arg Gly Gly Ala Arg Arg Pro Gly Arg
 45 100 105 110
 Ala Ala Ala Leu Thr Gln Gln Leu Xaa Gly Ala Gln Arg Asp Leu Glu
 115 120 125
 50 Ala Gly Gln Pro Thr Val Arg Thr Gln Leu Ser Glu Leu Arg
 130 135 140

55 (2) INFORMATION FOR SEQ ID NO: 239:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Asp Pro Glu Ala Ala Asp Ser Gly Glu Pro Gln Asn Lys Arg Thr Pro
 1 5 10 15
 Asp Leu Pro Glu Glu Glu Tyr Val Lys Glu Glu Ile Gln Glu Asn Glu
 20 25 30
 Glu Ala Val Lys Lys Met Leu Val Glu Ala Thr Arg Glu Phe Glu Glu
 35 40 45
 Val Val Val Asp Glu Ser
 50

15

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Gln Lys Leu Lys Arg Lys Ala Glu Glu Asp Pro Glu Ala Ala Asp Ser
 1 5 10 15
 Gly Glu Pro Gln Asn Lys Arg Thr Pro Asp Leu Pro Glu Glu Glu Tyr
 20 25 30
 Val Lys Glu Glu Ile Gln Glu Asn Glu Glu Ala Val Lys Lys Met Leu
 35 40 45
 Val Glu Ala Thr Arg Glu Phe Glu Glu Val Val Val Asp Glu Ser
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 241:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Lys Ala Met Glu Lys Ser Ser Leu Thr Gln His Ser Trp Gln Ser Leu
 1 5 10 15
 Lys Asp Arg Tyr Leu Lys His Leu Arg Gly Gln Glu His Lys Tyr Leu
 20 25 30
 Leu Gly Asp Ala Pro Val Ser Pro Ser Ser Gln Lys Leu Lys Arg Lys
 35 40 45
 Ala Glu Glu Asp Pro Glu Ala Ala Asp Ser Gly Glu Pro Gln Asn Lys
 50 55 60
 Arg Thr Pro Asp Leu Pro Glu Glu Glu Tyr Val Lys Glu Glu Ile Gln
 65 70 75 80

55

60

339

Glu Asn Glu Glu Ala Val Lys Lys Met Leu Val Glu Ala Thr Arg Glu
85 90 95

5 Phe Glu Glu Val Val Val Asp Glu Ser Pro Pro Asp Phe Glu Ile His
100 105 110

Ile

10

(2) INFORMATION FOR SEQ ID NO: 242:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

20

Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr Ile
1 5 10 15

25

Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp Phe
20 25 30

Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met Leu
35 40 45

30

Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu Ser
50 55 60

Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser Gly
65 70 75 80

35

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Thr
85 90 95

40

Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val Phe
100 105 110

Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr Ala
115 120 125

45

Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr Arg
130 135 140

Val Leu Phe Ile
145

50

(2) INFORMATION FOR SEQ ID NO: 243:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

60

340

Ala Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys
 1 5 10 15

5 Trp Ile Leu Ile Val Arg Phe Ser
 20

(2) INFORMATION FOR SEQ ID NO: 244:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Met Lys His Leu Ser Ala Trp Asn Phe Thr Lys Leu Thr Phe Leu Gln
 1 5 10 15

20 Leu Trp Glu Ile Phe Glu Gly Ser Val Glu Asn Cys Gln Thr Leu Thr
 20 25 30

Ser Tyr Ser Lys Leu Gln Ile Lys Tyr Thr Phe Ser Arg Gly Ser Thr
 35 40 45

25

Phe Tyr Ile
 50

30

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

40 Phe Ser Ser Asp Phe Arg Thr Ser Pro Trp Glu Ser Arg Arg Val Glu
 1 5 10 15

Ser Lys Ala Thr Ser Ala Arg Cys Gly Leu Trp Gly Ser Gly Pro Arg
 20 25 30

45 Arg Arg Pro Ala Ser Gly Met Phe Arg Gly Leu Ser Ser Trp Leu Gly
 35 40 45

Leu Gln Gln Pro Val Ala Gly Gly Gly Gln Pro Asn Gly Asp Ala Pro
 50 55 60

50

Pro Glu Gln Pro Ser Glu Thr Val Ala Glu Ser Ala Glu Glu Glu Leu
 65 70 75 80

Gln Gln Ala Gly Asp Gln Glu Leu Leu His Gln Ala Lys Asp Phe Gly
 85 90 95

55

Asn Tyr Leu Phe Asn Phe Ala Ser Ala Ala Thr Lys Lys Ile Thr Glu
 100 105 110

60 Ser Val Ala Glu Thr Ala Gln Thr Ile Lys Lys Ser Val Glu Glu Gly

341

115 120 125
 Lys Ile Asp Gly Ile Ile Asp Lys Thr Ile Ile Gly Asp Phe Gln Lys
 130 135 140
 5
 Glu Gln Lys Lys Phe Val Glu Glu Gln His Thr Lys Lys Ser Glu Ala
 145 150 155 160
 10
 Ala Val Pro Pro Trp Val Asp Thr Asn Asp Glu Glu Thr Ile Gln Gln
 165 170 175
 Gln Ile Leu Ala Leu Ser Ala Asp Lys Arg Asn Phe Leu Arg Asp Pro
 180 185 190
 15
 Pro Ala Gly Val Gln Phe Asn Phe Asp Phe Asp Gln Met Tyr Pro Val
 195 200 205
 20
 Ala Leu Val Met Leu
 210

(2) INFORMATION FOR SEQ ID NO: 246:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

30
 Met Arg Phe Ala Leu Val Pro Lys Leu Val Lys Glu Glu Val Phe Trp
 1 5 10 15
 35
 Arg Asn Tyr Phe Tyr Arg Val Ser Leu Ile Lys Gln Ser Ala Gln Leu
 20 25 30
 Thr Ala Leu Ala Ala Gln Gln Gln Ala Ala Gly Lys Gly Gly Glu Glu
 35 40 45
 40 Gln

(2) INFORMATION FOR SEQ ID NO: 247:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 50 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

55
 Ser Thr Ser Pro Gly Val Ser Glu Phe Val Ser Asp Ala Phe Asp Ala
 1 5 10 15
 Cys Asn Leu Asn Gln Glu Asp Leu Arg Lys Glu Met Glu Gln Leu Val
 20 25 30
 60
 Leu Asp Lys Lys Gln Glu Glu Thr Ala Val Leu Glu Glu Asp Ser Ala
 35 40 45

342

Asp Trp Glu Lys Glu Leu Gln Gln Glu Leu Gln Glu Tyr Glu Val Val
 50 55 60

5 Thr Glu Ser Glu Lys Arg Asp Glu Asn Trp Asp Lys
 65 70 75

10 (2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Ser Pro Trp Glu Ser Arg Arg Val Glu Ser Lys Ala Thr Ser Ala Arg
 1 5 10 15

20

Cys Gly Leu Trp Gly Ser Gly Pro Arg Arg Arg Pro Ala Ser Gly Met
 20 25 30

25

Phe Arg Gly Leu Ser Ser Trp Leu Gly Leu Gln Gln Pro Val Ala Gly
 35 40 45

Gly Gly Gln Pro Asn Gly Asp Ala Pro Pro Glu Gln Pro Ser
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

40 Pro Val Ala Gly Gly Gly Gln Pro Asn Gly Asp Ala Pro Pro Glu Gln
 1 5 10 15

Pro Ser Glu Thr Val Ala Glu Ser Ala Glu Glu Glu Leu Gln Gln Ala
 20 25 30

45

Gly Asp Gln Glu Leu Leu His Gln Ala Lys Asp Phe Gly Asn Tyr Leu
 35 40 45

50

Phe Asn Phe Ala Ser Ala Ala Thr Lys Lys Ile Thr Glu Ser Val Ala
 50 55 60

Glu
 65

55

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

60

343

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

5 Phe Gln Lys Glu Gln Lys Lys Phe Val Glu Glu Gln His Thr Lys Lys
 1 5 10 15

Ser Glu Ala Ala Val Pro Pro Trp Val Asp Thr Asn Asp Glu Glu Thr
 20 25 30

10 Ile Gln Gln Gln Ile Leu Ala Leu Ser Ala Asp Lys Arg Asn Phe Leu
 35 40 45

Arg Asp Pro Pro Ala Gly Val Gln Phe Asn Phe Asp Phe Asp Gln Met
 15 50 55 60

Tyr Pro Val Ala Leu Val Met Leu
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

25 Pro Phe Ile Cys Val Ala Arg Asn Pro Val Ser Arg Asn Phe Ser Ser
 1 5 10 15

Pro Ile Leu Ala Arg Lys Leu Cys Glu Gly Ala Ala
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

40 Lys Glu Asp Pro Ala Asn Thr Val Tyr Ser Thr Val Glu Ile Pro Lys
 1 5 10 15

Lys Met Glu Asn Pro His Ser Leu Leu Thr Met Pro Asp Thr Pro Arg
 50 20 25 30

Leu

55

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

60

344

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

5 Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu Ala Gln
 1 5 10 15
 Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp Val Thr
 20 25 30
 10 Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly Lys Phe
 35 40 45
 Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val Ala Ser
 15 50 55 60
 Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu Asp Phe
 65 70 75 80
 20 Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val Ile Arg
 85 90 95
 Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly Gly Gln
 100 105 110
 25 Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu Gly Gln
 115 120 125
 Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val Gly Met
 30 130 135 140
 Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg Val Met
 145 150 155 160
 35 Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser Leu Pro
 165 170 175
 Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro Ser Arg
 180 185 190
 40 Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile Ile Glu
 195 200 205
 Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala Ile Arg
 45 210 215 220
 Met Gln Pro
 225

50

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

60 Ser Val Ala Ala Phe Glu Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala

345

1 5 10 15
 Ser Lys Gly Gly Ile Val Gly Met Thr Leu Pro Ile Ala
 20 25

5

(2) INFORMATION FOR SEQ ID NO: 255:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

15

Ala Arg Arg Ser Gly Ala Glu Leu Ala Trp Asp Tyr Leu Cys Arg Trp
 1 5 10 15

20

Ala Gln Lys His Lys Asn Trp Arg Phe Gln Lys Thr Arg Gln Thr Trp
 20 25 30

Leu Leu Leu His Met Tyr Asp Ser Asp Lys Val Pro Asp Glu His Phe
 35 40 45

25

Ser Thr Leu Leu Ala Tyr Leu Glu Gly Leu Gln Gly Arg
 50 55 60

(2) INFORMATION FOR SEQ ID NO: 256:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

His Pro Ile Glu Trp Ala Ile Asn Ala Ala Thr Leu Ser Gln Phe Tyr
 1 5 10 15

40

Ile Asn Lys Leu Cys Phe
 20

45

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Cys Trp Ile Lys Tyr Cys Leu Thr Leu Met Gln Asn Ala Gln Leu Ser
 1 5 10 15

55

Met Gln Asp Asn Ile Gly
 20

60

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Lys Val Ser Tyr Leu Arg Pro Leu Asp Phe Glu Glu Ala Arg Glu Leu
 1 5 10 15

Phe Leu Leu Gly Gln His Tyr Val Phe
 20 25

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Met Glu Arg Arg Cys Lys Met His Lys Arg Xaa Ile Ala Met Leu Glu
 1 5 10 15

Pro Leu Thr Val Asp Leu Asn Pro Gln
 20 25

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Ser His Ile Val Lys Lys Ile Asn Asn Leu Asn Lys Ser Ala Leu Lys
 1 5 10 15

Tyr Tyr Gln Leu Phe Leu Asp
 20

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Phe Thr His Leu Ser Thr Cys Leu Leu Ser Leu Leu Leu Val Arg Met
 1 5 10 15

Ser Gly Phe Leu Leu Leu Ala Arg Ala Ser Pro Ser Ile Cys Ala Leu

347

20 25 30

Asp Ser Ser Cys Phe Val Gln Glu Tyr Cys Ser Ser Tyr Ser Ser Ser
35 40 45

5 Cys Phe Leu His Gln His Phe Pro Ser Leu Leu Asp His Leu Cys Gln
50 55 60

10

(2) INFORMATION FOR SEQ ID NO: 262:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Phe Leu Leu Leu Ala Arg Ala Ser Pro Ser Ile Cys Ala Leu Asp Ser
1 5 10 15

25

Ser Cys Phe Val Gln Glu Tyr
20

30

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Pro Asp Gly Arg Val Thr Asn Ile Pro Gln Gly Met Val Thr Asp Gln
1 5 10 15

40

Phe Gly Met Ile Gly Leu Leu Thr Phe Ile Arg Ala Ala Glu Thr Asp
20 25 30

45

Pro Gly Met Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr Leu Gly
35 40 45

Leu Asn Leu Asn Ser
50

50

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

60

Glu Asp Leu Leu Phe Tyr Leu Tyr Tyr Met Asn Gly Gly Asp Val Leu

348

1 5 10 15
 Gln Leu Leu Ala Ala Val Glu Leu Phe Asn Arg Asp Trp Arg Tyr His
 20 25 30
 5 Lys Glu Glu Arg Val Trp Ile Thr Arg
 35 40

10

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

15

20

Val His Leu Ala Leu Gly Ser Asp Leu Thr Thr Leu Gly Leu Asn Leu
 1 5 10 15
 Asn Ser Pro Glu Asn Leu Tyr Pro
 20

25

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

30

35

His Asn Glu Asp Phe Pro Ala Leu Pro Gly Ser
 1 5 10

40

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

45

50

Gly Arg Ile Ile Asp Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu
 1 5 10 15
 Leu Gly Gln Lys Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp
 20 25 30

55

Met Cys Val Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala
 35 40 45
 Tyr Gly Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val
 50 55 60

60

Gln Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg

349

65

70

75

5 (2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp Thr Ser
 1 5 10 15

15

20

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

Cys Glu Ser Pro Glu Ser Pro Ala Gln Pro Ser Gly Ser Ser Leu Pro
 1 5 10 15

30

Ala Trp Tyr His
 20

35

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Glu Glu Ala Gly Ala Gly Arg Arg Cys Ser His Gly Gly Ala Arg Pro
 1 5 10 15

45

Ala Gly Leu Gly Asn Glu Gly Leu Gly Leu Gly Gly Asp Pro Asp His
 20 25 30

50

Thr Asp Thr Gly Ser Arg Ser Lys Gln Arg Ile Asn Asn Trp Lys Glu
 35 40 45

55

Ser Lys His Lys Val Ile Met Ala Ser Ala Ser Ala Arg Gly Asn Gln
 50 55 60

Asp Lys Asp Ala His Phe Pro Pro Pro Ser Lys Gln Ser Leu Leu Phe
 65 70 75 80

60

Cys Pro Lys Ser Lys Leu His Ile His Arg Ala Glu Ile Ser Lys

350

85

90

95

5 (2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

Ser Lys Gln Arg Ile Asn Asn Trp Lys Glu Ser Lys His Lys Val Ile
1 5 10 15

15

Met Ala Ser Ala Ser Ala Arg
20

20

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

Leu Phe His Trp Ala Cys Leu Asn Glu Arg Ala Ala Gln Leu Pro Arg
1 5 10 15

30

Asn Thr Ala Xaa Ala Gly Tyr Gln Cys Pro Ser Cys Asn Gly Pro Ser
20 25 30

35

40 (2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

Phe Tyr Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr
1 5 10 15

50

Lys Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His
20 25 30

Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn Glu
35 40 45

55

Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr Lys Ala
50 55 60

60

Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro Thr Leu Ala

351

[illegible]

25 (2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

30 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

[illegible]

50 (2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

55 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

60 Asn Val Arg Ala Leu Leu His Arg Met Pro Glu Pro Pro Lys Ile Asn
1 5 10 15

352

Thr Ala Lys Phe Asn Asn Asn Lys Arg Lys Asn Leu Ser Leu
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

10

15

Asn Thr Asn Gln Arg Glu Ala Leu Gln Tyr Ala Lys Asn Phe Gln Pro
 1 5 10 15

Phe Ala Leu Asn His Gln Lys Asp Ile Gln Val Leu Met Gly Ser Leu
 20 25 30

20

Val Tyr Leu Arg Gln Gly Ile Glu Asn Ser Pro Tyr Val His Leu Leu
 35 40 45

25

Asp Ala Asn Gln Trp Ala Asp Ile Cys Asp Ile Phe Thr Arg Asp Ala
 50 55 60

Cys Ala Leu Leu Gly Leu Ser Val Glu Ser Pro Leu Ser Val Ser Phe
 65 70 75 80

30

Ser Ala Gly Cys Val Ala Leu Pro Ala Leu Ile Asn Ile Lys Ala Val
 85 90 95

Ile Glu Gln Arg Gln Cys Thr Gly Val Trp Asn Gln Lys Asp Glu Leu
 100 105 110

35

Pro Ile Glu Val Asp Leu Gly Lys Lys Cys Trp Tyr His Ser Ile Phe
 115 120 125

40

Ala Cys Pro Ile Leu Arg Gln Gln Thr Thr Asp Asn Asn Pro Pro Met
 130 135 140

Lys Leu Val Cys Gly His Ile Ile Ser Arg Asp Ala Leu Asn Lys Met
 145 150 155 160

45

Phe Asn Gly Ser Lys Leu Lys Cys Pro Tyr Cys Pro Met Glu Gln Ser
 165 170 175

Pro Gly Asp Ala Lys Gln Ile Phe Phe
 180 185

50

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

55

60

353

Ser Tyr Leu Ser Ala Cys Phe Ala Gly Cys Asn Ser Thr Asn Leu Thr
 1 5 10 15
 Gly Cys Ala Cys Leu Thr Thr Val Pro Ala Glu Asn Ala Thr Val Val
 5 20 25 30
 Pro Gly Lys Cys Pro Ser Pro Gly Cys Gln Glu Ala Phe Leu Thr Phe
 35 40 45
 10 Leu Cys Val Met Cys Ile Cys Ser Leu Ile Gly Ala Met Ala Arg His
 50 55 60
 Pro
 65
 15

(2) INFORMATION FOR SEQ ID NO: 278:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:
 25 Pro Ser Val Ile Ile Leu Ile Arg Thr Val Ser Pro Glu Leu Lys Ser
 1 5 10 15
 Tyr Ala Leu Gly Val Leu Phe Leu Leu Leu Arg Leu Leu Gly Phe Ile
 30 20 25 30
 Pro Pro Pro Leu Ile Phe Gly Ala Gly Ile Asp Ser Thr Cys Leu Phe
 35 35 40 45
 Trp Ser Thr Phe Cys Gly Glu Gln Gly Ala Cys Val Leu Tyr Asp Asn
 50 55 60
 Val Val Tyr Arg Tyr Leu Tyr Val Ser Ile Ala Ile Ala Leu Lys Ser
 65 70 75 80
 40 Phe Ala Phe Ile

45

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 amino acids
 50 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:
 Gln Ser Leu Phe Thr Arg Phe Val Arg Val Gly Val Pro Thr Val Asp
 55 1 5 10 15
 Leu Asp Ala Gln Gly Arg Ala Arg Ala Ser Leu Cys Xaa Xaa Tyr Asn
 20 25 30
 60 Trp Arg Tyr Lys Asn Leu Gly Asn Leu Pro His Val Gln Leu Leu Pro

354

35 40 45
 Glu Phe Ser Thr Ala Asn Ala Gly Leu Leu Tyr Asp Phe Gln Leu Ile
 50 55 60
 5 Asn Val Glu Asp Phe Gln Gly Val Gly Glu Ser Glu Pro Asn Pro Tyr
 65 70 75 80
 10 Phe Tyr Gln Asn Leu Gly Glu Ala Glu Tyr Val Val Ala Leu Phe Met
 85 90 95
 Tyr Met Cys Leu Leu Gly Tyr Pro Ala Asp Lys Ile Ser Ile Leu Thr
 100 105 110
 15 Thr Tyr Asn Gly Gln Lys His Leu Ile Arg Asp Ile Ile Asn Arg Arg
 115 120 125
 Cys Gly Asn Asn Pro Leu Ile Gly Arg Pro Asn Lys Val Thr Thr Val
 130 135 140
 20 Asp Arg Phe Gln Gly Gln Gln Asn Asp Tyr Ile Leu Leu Ser Leu Val
 145 150 155 160
 25 Arg Thr Arg Ala Val Gly His Leu Arg Asp Val Arg Arg Leu Val Val
 165 170 175
 Ala Met Ser Arg Ala Arg
 180

30

(2) INFORMATION FOR SEQ ID NO: 280:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

40 Leu Val Lys Glu Ala Lys Ile Ile Ala Met Thr Cys Thr His Ala Ala
 1 5 10 15
 Leu Lys Arg His Asp Leu Val Lys Leu Gly Phe Lys Tyr Asp Asn Ile
 20 25 30
 45 Leu Met Glu Ala Ala Gln Ile Leu Glu Ile Glu Thr Phe Ile Pro
 35 40 45
 50 Leu Leu Leu Gln Asn Pro Gln Asp Gly Phe Ser Arg Leu Lys Arg Trp
 50 55 60
 Ile Met Ile Gly Asp His His Gln Leu Pro Pro Val Ile
 65 70 75

55

(2) INFORMATION FOR SEQ ID NO: 281:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids

355

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

5 Asp Thr Tyr Pro Asn Glu Glu Lys Gln Gln Glu Arg Val Phe Pro Xaa
 1 5 10 15
 Xaa Ser Ala Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Glu Arg
 20 25 30
 10 Asp Gly Arg Pro Thr Glu Leu Gly Gly Cys Xaa Ala Ile Val Arg Asn
 35 40 45
 Leu His Tyr Asp Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu
 15 50 55 60
 Thr Ile Met Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile
 65 70 75 80
 20 Glu Val Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser
 85 90 95
 Ser Ile Thr Gly Asp Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys
 100 105 110
 25 Leu Phe Glu Leu Thr Val Glu Arg Thr Pro Glu Glu Glu
 115 120 125

30

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

40 Leu Lys Arg Glu His Ser Leu Ser Lys Pro Tyr Gln Gly Val Gly Thr
 1 5 10 15
 Gly Ser Ser Ser Leu Trp Asn Leu Met Gly Asn Ala Met Val Met Thr
 20 25 30
 45 Gln Tyr Ile Arg Leu Thr Pro Asp Met Gln Ser Lys Gln Gly Ala Leu
 35 40 45
 Trp Asn Arg Val Pro Cys Phe Leu Arg Asp Trp Glu Leu Gln Val His
 50 55 60
 50 Phe Lys Ile His Gly Gln Gly Lys Lys Asn Leu His Gly Asp Gly Leu
 65 70 75 80
 Ala Ile Trp Tyr Thr
 55 85

60

(2) INFORMATION FOR SEQ ID NO: 283:

356

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

Pro Gly Thr Leu Gln Cys Ser Ala Leu His His Asp Pro Gly Cys Ala
 1 5 10 15
 10 Asn Cys Ser Arg Phe Cys Arg Asp Cys Ser Pro Pro Ala Cys Gln Cys
 20 25 30

15

(2) INFORMATION FOR SEQ ID NO: 284:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

Phe Leu Tyr Asp Val Leu Met Xaa His Glu Ala Val Met Arg Thr His
 1 5 10 15
 30 Gln Ile Gln Leu Pro Asp Pro Glu Phe Pro Ser
 20 25

(2) INFORMATION FOR SEQ ID NO: 285:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

Gly Trp Tyr Trp Cys Gly
 1 5

45

(2) INFORMATION FOR SEQ ID NO: 286:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

55 Met Lys Val Gly Ala Arg Ile Arg Val Lys Met Ser Val Asn Lys Ala
 1 5 10 15
 His Pro Val Val Ser Thr His Trp Arg Trp Pro Ala Glu Trp Pro Gln
 20 25 30

60

357

Met Phe Leu His Leu Ala Gln Glu Pro Arg Thr Glu Val Lys Ser Arg
 35 40 45

5 Pro Leu Gly Leu Ala Gly Phe Ile Arg Gln Asp Ser Lys Thr Arg Lys
 50 55 60

Pro Leu Glu Gln Glu Thr Ile Met Ser Ala Ala Asp Thr Ala Leu Trp
 65 70 75 80

10 Pro Tyr Gly His Gly Asn Arg Glu His Gln Glu Asn Glu Leu Gln Lys
 85 90 95

Tyr Leu Gln Tyr Lys Asp Met His Leu Leu Asp Ser Gly Gln Ser Leu
 100 105 110

15 Gly His Thr His Thr Leu Gln Gly Ser His Asn Leu Thr Ala Leu Asn
 115 120 125

Ile

20

(2) INFORMATION FOR SEQ ID NO: 287:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

Ser Leu His Lys Asn Ser Val Ser Gln Ile Ser Val Leu Ser Gly Gly
 1 5 10 15

35 Lys Ala Lys Cys Ser Gln Phe Cys Thr Thr Gly Met Asp Gly Gly Met
 20 25 30

Ser Ile Trp Asp Val Lys Ser Leu Glu Ser Ala Leu Lys Asp Leu Lys
 35 40 45

40 Ile

45

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

50

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

Glu Ala Ser Lys Ser Ser His Ala Gly Leu Asp Leu Phe Ser Val Ala
 55 1 5 10 15

Ala Cys His Arg Phe
 20

60

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

5 Tyr Met Gly Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe
 1 5 10 15

Glu Arg Ser Phe Thr
 20

15

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

20

25

Val Thr Gly Ile Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg
 1 5 10 15

30

Val Gly Leu Leu Gln Tyr Ser Thr Gln Val His
 20 25

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

35

40

Thr Glu Phe Thr Leu Arg Asn Phe Asn Ser Ala Lys Asp Met Lys Lys
 1 5 10 15

45

Ala Val Ala His Met Lys Tyr Met
 20

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

50

55

Gly Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg
 1 5 10 15

60

359

Ser Phe Thr Gln Gly Glu Gly Ala Arg Pro Phe
 20 25

5

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

10

15

Ser Thr Arg Val Pro Arg Ala Ala Ile Val Phe Thr Asp Gly Arg Ala
 1 5 10 15

Gln Asp Asp Val Ser Glu Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile
 20 25 30

20

Thr Met Tyr Ala Val Gly Val Gly Lys Ala Ile Glu
 35 40

25

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

30

Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro Thr Asn Lys His Leu Phe
 1 5 10 15

35

Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu Ile Ser Glu Lys Leu Lys
 20 25 30

40

Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 35 40

45

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

50

Thr Gln Arg Leu Glu Glu Met Thr Gln Arg Met
 1 5 10

55

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

60

360

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

5 Pro Gln Gly Cys Pro Glu Gln Pro Leu His
1 5 10

10 (2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Arg Cys Lys Lys Cys Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile
1 5 10 15
20 Asp Gly Ser Lys Ser Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln
20 25 30
25 Phe

30 (2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

Met Ala Ala Leu Leu Leu Arg His Val Gly Arg His Cys Leu Arg Ala
1 5 10 15
40 His Phe Ser Pro Gln Leu Cys Ile Arg Asn Ala Val Pro Leu Gly Thr
20 25 30
Thr Ala Lys Glu Glu Met Glu Arg Phe Trp Asn Lys Asn Ile Gly Ser
35 40 45
45 Asn Arg Pro Leu Ser Pro His Ile Thr Ile Tyr Ser
50 55 60

50 (2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

60 Val Phe Pro Leu Met Tyr His Thr Trp Asn Gly Ile Arg His Leu Met
1 5 10 15

Trp Asp Leu Gly Lys Gly Leu Lys Ile Pro Gln Leu Tyr Gln Ser Gly
 20 25 30

5

10 (2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ala Ala Leu Leu Leu Arg His Val Gly Arg His Cys Leu Arg Ala
 1 5 10 15

20

His

25

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Val Lys Ser Leu Cys Leu Gly Pro Ala Leu Ile His Thr Ala Lys Phe
 1 5 10 15

35

Ala Leu

40

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

Val Phe Pro Leu Met Tyr His Thr Trp Asn Gly Ile Arg His Leu Met
 1 5 10 15

50

Trp Asp Leu Gly Lys Gly Leu
 20

55

(2) INFORMATION FOR SEQ ID NO: 303:

60

(i) SEQUENCE CHARACTERISTICS:

362

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

5 Arg Val Trp Asp Val Arg Pro Phe Ala Pro Lys Glu Arg Cys Val Lys
 1 5 10 15

10 Ile Phe Gln Gly Asn Val
 20

(2) INFORMATION FOR SEQ ID NO: 304:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

His Asn Phe Glu Lys Asn Leu Leu Arg Cys Ser Trp Ser Pro Asp Gly
 1 5 10 15

25 Ser Lys Ile Ala Ala Gly Ser Ala Asp Arg Phe Val Tyr Val
 20 25 30

30

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

Trp Asp Thr Thr Ser Arg Arg Ile Leu Tyr Lys Leu Pro Gly His Ala
 1 5 10 15

40 Gly Ser Ile Asn Glu Val Ala Phe His Pro Asp Glu Pro Ile
 20 25 30

45

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

Val Arg Gly Arg Thr Val Leu Arg Pro Gly Leu Asp Ala Glu Pro Glu
 1 5 10 15

55 Leu Ser Pro Glu
 20

60

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

10 Glu Gln Arg Val Leu Glu Arg Lys Leu Lys Lys Glu Arg Lys Lys Glu
1 5 10 15

Glu Arg Gln

15

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

25 Arg Leu Arg Glu Ala Gly Leu Val Ala Gln His Pro Pro
1 5 10

30

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

40 Gly Arg Ile Pro Ala Pro Ala Pro Ser Val Pro Ala Gly Pro Asp Ser
1 5 10 15

Arg

45

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

55 Thr Gly Cys Val Leu Val Leu Ser Arg Asn Phe Val Gln Tyr Ala Cys
1 5 10 15

Phe Gly Leu Phe Gly Ile Ile Ala Leu Gln Thr Ile Ala Tyr Ser Ile
20 25 30

60

Leu Trp Asp Leu Lys Phe Leu Met Arg Asn
 35 40

5

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

15 Ser Arg Ser Glu Gly Lys Ser Met Phe Ala Gly Val Pro Thr Met Arg
 1 5 10 15
 Glu Ser Ser Pro Lys Gln Tyr Met Gln Leu Gly Gly Arg Val Leu Leu
 20 25 30
 20 Val Leu Met Phe Met Thr Leu Leu His Phe Asp Ala Ser Phe Phe Ser
 35 40 45
 Ile Val Gln Asn Ile Val Gly
 50 55

25

(2) INFORMATION FOR SEQ ID NO: 312:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

35

Gly Thr Ala Glu Asp Phe Ala Asp Gln Phe Leu Arg Val Thr Lys Gln
 1 5 10 15
 40 Tyr Leu Pro His Val Ala Arg Leu Cys Leu Ile Ser Thr Phe Leu Glu
 20 25 30
 Asp Gly Ile Arg Met Trp Phe Gln Trp Ser Glu Gln Arg Asp Tyr Ile
 35 40 45
 45 Asp Thr Thr Trp Asn Cys Gly Tyr Leu Leu Ala Ser
 50 55 60

50

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

55

Ala Ser Phe Leu Leu Ser Arg Thr Ser Trp Gly Thr Ala Leu Met Ile
 1 5 10 15

60

Leu

5

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

15

Leu Met Arg Asn Glu Ser Arg Ser
1 5

20

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Ala Ser Phe Leu Leu Ser Arg Thr Ser Trp Gly Thr Ala
1 5 10

30

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

40

Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met
1 5 10 15

45

Met Ser Ser Phe
20

(2) INFORMATION FOR SEQ ID NO: 317:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

55

Asp Pro Arg Arg Pro Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser
1 5 10 15

60

Glu Cys Asn Pro Ala Leu Asp Asp Pro Thr Pro
20 25

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly Leu Met
1 5 10 15

Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu Gln Asn Pro Gln
1 5 10 15

Pro Met Thr Pro Pro Trp
20

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Ala Ala Gly Asp Gly Asp Val Lys Leu Gly Thr Leu Gly Ser Gly Ser
1 5 10 15

Glu Ser Ser Asn Asp Gly Gly Ser Glu Ser Pro Gly Asp Ala Gly Ala
20 25 30

Ala Ala Xaa Gly Gly Gly Trp Ala Ala Ala Ala Leu Ala Leu Leu Thr
35 40 45

Gly Gly Gly Glu
50

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

367

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

5
 Ala Ala Asp Asn Tyr Gly Ile Pro Arg Ala Cys Arg Asn Ser Ala Arg
 1 5 10 15

10
 Ser Tyr Gly Ala Ala Trp Leu Leu Leu Xaa Pro Ala Gly Ser Ser Arg
 20 25 30

Val Glu Pro Thr Gln Asp Ile Ser Ile Ser Asp Gln Leu Gly Gly Gln
 35 40 45

15
 Asp Val Pro Val Phe Arg Asn Leu Ser Leu Leu Val Val Gly Val Gly
 50 55 60

Ala Val Phe Ser Leu Leu Phe His Leu Gly Thr Arg Glu Arg Arg Arg
 65 70 75 80

20
 Pro His Ala Xaa Glu Pro Gly Glu His Thr Pro Leu Leu Ala Pro Ala
 85 90 95

25
 Thr Ala Gln Pro Leu Leu Leu Trp Lys His Trp Leu Arg Glu Xaa Ala
 100 105 110

Phe Tyr Gln Val Gly Ile Leu Tyr Met Thr Thr Arg Leu Ile Val Asn
 115 120 125

30
 Leu Ser Gln Thr Tyr Met Ala Met Tyr Leu Thr Tyr Ser Leu His Leu
 130 135 140

Pro Lys Lys Phe Ile Ala Thr Ile Pro Leu Val Met Tyr Leu Ser Gly
 145 150 155 160

35
 Phe Leu Ser Ser Phe Leu Met Lys Pro Ile Asn Lys Cys Ile Gly Arg
 165 170 175

40
 Asn

(2) INFORMATION FOR SEQ ID NO: 322:

45
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

50
 Arg Ile Thr Asp Asn Pro Glu Gly Lys Trp Leu Gly Arg Thr Ala Arg
 1 5 10 15

55
 Gly Ser Tyr Gly Tyr Ile Lys Thr Thr Ala Val Glu Ile Xaa Tyr Asp
 20 25 30

Ser Leu Lys Leu Lys Lys Asp Ser Leu Gly Ala Pro Ser Arg Pro Ile
 35 40 45

60
 Glu Asp Asp Gln Glu Val Tyr Asp Asp Val Ala Glu Gln Asp Asp Ile

[illegible]

40

(A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45

50

369

65 70 75 80

Val Leu Gly His Phe Pro Tyr Pro Asp Pro Ser Gln Trp Thr Asp Glu
85 90 95

5

Glu Leu Gly Ile Pro Pro Asp Asp Glu Asp
100 105


370

Applicant's or agent's file reference number	004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>73</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 7, 1997	Accession Number 97923
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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<input checked="checked" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer 	Authorized officer

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>73</u> line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit	May 22, 1997
Accession Number	209071
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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372

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>73</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit February 25, 1998	Accession Number 209641
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	

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373

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>75</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>July 24, 1997</u>	Accession Number <u>209179</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	

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374

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>77</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>March 7, 1997</u>	Accession Number <u>97924</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	

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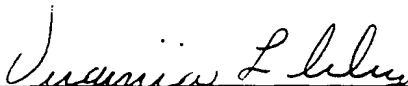
375

Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 80, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 13, 1997	Accession Number 97958
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>80</u> . line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>May 22, 1997</u>	Accession Number <u>209072</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>80</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>10801 University Boulevard</u> <u>Manassas, Virginia 20110-2209</u> <u>United States of America</u>	
Date of deposit <u>September 4, 1997</u>	Accession Number <u>209235</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 84, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit August 28, 1997	Accession Number 209226
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 84, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit March 13, 1997	Accession Number 97957
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications. e.g., "Accession Number of Deposit")	

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Applicant's or agent's file reference number	Z004PCT	International application	Unassigned
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 84, line N/A	
B. IDENTIFICATION OF DEPOSIT	
Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit May 22, 1997	Accession Number 209073
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

5 (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

10 (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

15 (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

20 (f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

10

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

15

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

20

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

25

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

30

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

35

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

5 12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

10 13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15 15. A method of making an isolated polypeptide comprising:
15 (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
15 (b) recovering said polypeptide.

20 16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

25 18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
25 (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
25 (b) diagnosing a pathological condition or a susceptibility to a pathological
30 condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
35 (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
35 (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- 5 (a) contacting the polypeptide of claim 11 with a binding partner; and
(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

10 22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
(b) isolating the supernatant;
(c) detecting an activity in a biological assay; and
15 (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/05311

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C12N5/10 C12N1/21 C07K14/47 C07K16/18
C12Q1/68 G01N33/50 G01N33/53 G01N33/68 A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	L. HILLIER ET AL.: "The WashU-Merck EST project" EMBL SEQUENCE DATABASE, 2 July 1995, HEIDELBERG, FRG, XP002068365 y187a06.r1 Homo sapiens cDNA clone 44938 5'; Accession no. H08241; ---	1-3, 7-11,21
X	L. HILLIER ET AL.: "The "WashU-Merck EST project" EMBL SEQUENCE DATABASE, 26 August 1995, HEIDELBERG, FRG, XP002068366 ym94e01.r1 Homo sapiens cDNA clone 166584 5', Accession no. R88485; ---	1-3, 7-11,21
A	WO 97 07198 A (GENETICS INSTITUT) 27 February 1997 see the whole document ---	1-23
-/-		

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

16. 09. 1998

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

HORNIG H.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/05311

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 97 04097 A (GENETICS INST) 6 February 1997 see the whole document ---	1-23
A	US 5 536 637 A (JACOBS KENNETH) 16 July 1996 see the whole document ---	1-23
A	JACOBS K ET AL: "A novel method for isolating eukaryotic cDNA clones encoding secreted proteins." KEYSTONE SYMPOSIUM ON DENDRITIC CELLS: ANTIGEN PRESENTING CELLS OF T AND B LYMPHOCYTES, TAOS, NEW MEXICO, USA, MARCH 10-16, 1995. JOURNAL OF CELLULAR BIOCHEMISTRY SUPPLEMENT 0 (21A). 1995. 19. ISSN: 0733-1959, XP002027246 abstract no. C1-207 see abstract ---	1-23
A	WO 90 14432 A (GENETICS INST) 29 November 1990 see the whole document ---	1-23
A	WO 96 17925 A (IMMUNEX CORP) 13 June 1996 see the whole document -----	1-23

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/ 05311

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claim 17 is directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1. Claims: (1-23) partially

-An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from SEQ ID no. 11; wherein said polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein encoding the sequence SEQ ID no.125 or the polypeptide encoded by the cDNA sequence included in ATCC Deposit nos: 97923/209071, which is hybridizable to SEQ ID no.11; a recombinant vector comprising said isolated nucleic acid molecule; a method of making a recombinant host cell comprising said isolated nucleic acid molecule; a recombinant host cell comprising said vector; an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence SEQ ID no. 125; an isolated antibody that binds specifically to said isolated polypeptide; a recombinant host cell that expresses said isolated polypeptide; a method of making said polypeptide; a method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of said polypeptide; a method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject using said polynucleotide and/or polypeptide sequence; a method for identifying a binding partner to said polypeptide; a gene corresponding to the cDNA sequence of SEQ ID no.11; a method for identifying an activity in a biological assay, by using the expression of SEQ ID no. 125;

Inventions 2 to 87. Claims: (12-23) partially

-Idem as subject 1 but limited to gene nos. 2 to 87 respectively cDNA clone sequences HAGFY16/HBMCF37/HFLQB16 to HCED021. (Invention 2 is limited to SEQ ID nos. 12,98,99,126,212 and 213; Invention 3 is limited to SEQ ID nos.13 and 127;; Invention 87 is limited to SEQ ID nos.97 and 211;)

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/05311

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9707198 A	27-02-97	US 5707829 A	13-01-98
		AU 6712396 A	18-02-97
		AU 6768596 A	12-03-97
		EP 0839196 A	06-05-98
		EP 0851875 A	08-07-98
		WO 9704097 A	06-02-97

WO 9704097 A	06-02-97	US 5707829 A	13-01-98
		AU 6712396 A	18-02-97
		EP 0839196 A	06-05-98
		AU 6768596 A	12-03-97
		EP 0851875 A	08-07-98
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